

## IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of  Avi Ashkenazi, et al.  Serial No.: Filed herewith  Filed: Herewith  For: <i>Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same</i>	Group Art Unit: Not yet assigned  Examiner: Not yet assigned  Express Mail No: EL 895 375 467 US Mailed: November 15, 2001
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CERTIFICATE RE: SEQUENCE LISTINGRESPONSE UNDER 37 CFR § 1.821(f) and (g)

Box: Patent Application  
 Assistant Commissioner of Patents  
 Washington, D.C. 20231

Sir:

I hereby state that the Sequence Listing submitted herewith is submitted in paper copy and a computer-readable diskette, and that the information recorded in computer readable form is identical to the written sequence listing. I further state that this submission includes no new matter.

Respectfully submitted,

GENENTECH, INC.

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09157

PATENT TRADEMARK OFFICE

Sequence Listing

<110> Avi J. Ashkenazi  
Kevin P. Baker  
David A. Botstein  
Luc Desnoyers  
Dan L. Eaton  
Napoleone Ferrara  
Sherman Fong  
Wei-Qiang Gao  
Hanspeter Gerber  
Mary E. Gerritsen  
Audrey Goddard  
Paul J. Godowski  
Austin L. Gurney  
Ivar J. Kljavin  
Jennie P. Mather  
Mary A. Napier  
James Pan  
Nicholas F. Paoni  
Margaret Ann Roy  
Timothy A. Stewart  
Daniel Tumas  
Colin K. Watanabe  
P.Mickey Williams  
William I. Wood  
Zemin Zang

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<210> 13

<211> 247

<212> PRT

<213> Homo Sapien

<400> 13

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Ala	Arg	Glu	Gln	His	Trp	Asp	Arg	Pro	Ser	Ala	Ser	Arg	Arg	Arg
	20								25					30
Ser	Ser	Pro	Ser	Lys	Asn	Arg	Gly	Leu	Cys	Asn	Gly	Asn	Leu	Val
				35					40					45
Asp	Ile	Phe	Ser	Lys	Val	Arg	Ile	Phe	Gly	Leu	Lys	Lys	Arg	Arg
					50				55					60

Leu Arg Arg Gln Asp Pro Gln Leu Lys Gly Ile Val Thr Arg Leu  
                   65                    70                    75  
 Tyr Cys Arg Gln Gly Tyr Tyr Leu Gln Met His Pro Asp Gly Ala  
                   80                    85                    90  
 Leu Asp Gly Thr Lys Asp Asp Ser Thr Asn Ser Thr Leu Phe Asn  
                   95                    100                  105  
 Leu Ile Pro Val Gly Leu Arg Val Val Ala Ile Gln Gly Val Lys  
                   110                  115                  120  
 Thr Gly Leu Tyr Ile Ala Met Asn Gly Glu Gly Tyr Leu Tyr Pro  
                   125                  130                  135  
 Ser Glu Leu Phe Thr Pro Glu Cys Lys Phe Lys Glu Ser Val Phe  
                   140                  145                  150  
 Glu Asn Tyr Tyr Val Ile Tyr Ser Ser Met Leu Tyr Arg Gln Gln  
                   155                  160                  165  
 Glu Ser Gly Arg Ala Trp Phe Leu Gly Leu Asn Lys Glu Gly Gln  
                   170                  175                  180  
 Ala Met Lys Gly Asn Arg Val Lys Lys Thr Lys Pro Ala Ala His  
                   185                  190                  195  
 Phe Leu Pro Lys Pro Leu Glu Val Ala Met Tyr Arg Glu Pro Ser  
                   200                  205                  210  
 Leu His Asp Val Gly Glu Thr Val Pro Lys Pro Gly Val Thr Pro  
                   215                  220                  225  
 Ser Lys Ser Thr Ser Ala Ser Ala Ile Met Asn Gly Gly Lys Pro  
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 Val Asn Lys Ser Lys Thr Thr  
                   245

<210> 14  
 <211> 2609  
 <212> DNA  
 <213> Homo Sapien

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 tgagcgctgt aatctgaacc agctgtgtcc agactgaggc cccatggca 150  
 ttgttaaca tacttagaaa atgaagtgtt catttttaac attcctcctc 200  
 caattggttt aatgctgaat tactgaagag ggctaagcaa aaccagggtgc 250  
 ttgcgctgag ggctctgcag tggctggag gaccccgccg ctctccccgt 300  
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ccgagggccc agaggaggcc gacgtgcccg agtcctccg ggggtccgc 400  
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tgccaggaat aaaaaggata ctcaactgtta ccattctggc tctctgtt 500  
ccaagccctg ggaatgcaca ggcacagtgc acgaatggct ttgacctgga 550  
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tgcattcccc ggacaaaccc tgtgtatcga gggccctact cgaaccctca 700  
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tgcagcagac gtgctacaat ttacaagggg gcttcaaatg catcgaccc 1400  
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ctgctgaacg tttccccaa gagtcagccc cgacttcctg actctcacct 1950  
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<210> 15  
<211> 448  
<212> PRT  
<213> Homo Sapien

<400> 15  
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Phe Asp Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu  
35 40 45  
Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val  
50 55 60  
Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val  
65 70 75  
Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Pro Tyr Ser Gly  
80 85 90

Pro	Tyr	Pro	Ala	Ala	Pro	Pro	Leu	Ser	Ala	Pro	Asn	Tyr	Pro	
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Thr	Ile	Ser	Arg	Pro	Leu	Ile	Cys	Arg	Phe	Gly	Tyr	Gln	Met	Asp
							110					115		120
Glu	Ser	Asn	Gln	Cys	Val	Asp	Val	Asp	Glu	Cys	Ala	Thr	Asp	Ser
							125					130		135
His	Gln	Cys	Asn	Pro	Thr	Gln	Ile	Cys	Ile	Asn	Thr	Glu	Gly	Gly
							140					145		150
Tyr	Thr	Cys	Ser	Cys	Thr	Asp	Gly	Tyr	Trp	Leu	Leu	Glu	Gly	Gln
							155					160		165
Cys	Leu	Asp	Ile	Asp	Glu	Cys	Arg	Tyr	Gly	Tyr	Cys	Gln	Gln	Leu
							170					175		180
Cys	Ala	Asn	Val	Pro	Gly	Ser	Tyr	Ser	Cys	Thr	Cys	Asn	Pro	Gly
							185					190		195
Phe	Thr	Leu	Asn	Glu	Asp	Gly	Arg	Ser	Cys	Gln	Asp	Val	Asn	Glu
							200					205		210
Cys	Ala	Thr	Glu	Asn	Pro	Cys	Val	Gln	Thr	Cys	Val	Asn	Thr	Tyr
							215					220		225
Gly	Ser	Leu	Ile	Cys	Arg	Cys	Asp	Pro	Gly	Tyr	Glu	Leu	Glu	Glu
							230					235		240
Asp	Gly	Val	His	Cys	Ser	Asp	Met	Asp	Glu	Cys	Ser	Phe	Ser	Glu
							245					250		255
Phe	Leu	Cys	Gln	His	Glu	Cys	Val	Asn	Gln	Pro	Gly	Thr	Tyr	Phe
							260					265		270
Cys	Ser	Cys	Pro	Pro	Gly	Tyr	Ile	Leu	Leu	Asp	Asp	Asn	Arg	Ser
							275					280		285
Cys	Gln	Asp	Ile	Asn	Glu	Cys	Glu	His	Arg	Asn	His	Thr	Cys	Asn
							290					295		300
Leu	Gln	Gln	Thr	Cys	Tyr	Asn	Leu	Gln	Gly	Gly	Phe	Lys	Cys	Ile
							305					310		315
Asp	Pro	Ile	Arg	Cys	Glu	Glu	Pro	Tyr	Leu	Arg	Ile	Ser	Asp	Asn
							320					325		330
Arg	Cys	Met	Cys	Pro	Ala	Glu	Asn	Pro	Gly	Cys	Arg	Asp	Gln	Pro
							335					340		345
Phe	Thr	Ile	Leu	Tyr	Arg	Asp	Met	Asp	Val	Val	Ser	Gly	Arg	Ser
							350					355		360
Val	Pro	Ala	Asp	Ile	Phe	Gln	Met	Gln	Ala	Thr	Thr	Arg	Tyr	Pro
							365					370		375
Gly	Ala	Tyr	Tyr	Ile	Phe	Gln	Ile	Lys	Ser	Gly	Asn	Glu	Gly	Arg

380	385	390
Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val		
395	400	405
Met Thr Arg Pro Ile Lys Gly Pro Arg Glu Ile Gln Leu Asp Leu		
410	415	420
Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg Gly Ser Ser		
425	430	435
Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe		
440	445	

<210> 16  
<211> 2447  
<212> DNA  
<213> Homo Sapien

<400> 16  
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tgcagagaag cagttgtttt gctggaagga gggagtgcgc gggctgcccc 150  
gggctcctcc ctgcccgcctc ctctcagtgg atggttccag gcaccctgtc 200  
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gagggtccgc ttgactaaga gtagcttgaa ggaggcacca tgcaaggagct 400  
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cccccgacg cttcccgacg cttccgtgct ctgcgctcgc tgcaactcaa 850  
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ccaaaaaaaaaaaaaaa gggcgccgc gactctagag tcgacct 2447

<210> 17

<211> 428

<212> PRT

<213> Homo Sapien

<400> 17

Met Gln Glu Leu His Leu Leu Trp Trp Ala Leu Leu Leu Gly Leu  
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Ala Gln Ala Cys Pro Glu Pro Cys Asp Cys Gly Glu Lys Tyr Gly  
20 25 30

Phe Gln Ile Ala Asp Cys Ala Tyr Arg Asp Leu Glu Ser Val Pro  
35 40 45

Pro Gly Phe Pro Ala Asn Val Thr Thr Leu Ser Leu Ser Ala Asn  
50 55 60

Arg Leu Pro Gly Leu Pro Glu Gly Ala Phe Arg Glu Val Pro Leu  
65 70 75

Leu Gln Ser Leu Trp Leu Ala His Asn Glu Ile Arg Thr Val Ala  
80 85 90

Ala Gly Ala Leu Ala Ser Leu Ser His Leu Lys Ser Leu Asp Leu  
95 100 105

Ser His Asn Leu Ile Ser Asp Phe Ala Trp Ser Asp Leu His Asn  
110 115 120

Leu Ser Ala Leu Gln Leu Leu Lys Met Asp Ser Asn Glu Leu Thr  
125 130 135

Phe Ile Pro Arg Asp Ala Phe Arg Ser Leu Arg Ala Leu Arg Ser  
140 145 150

Leu Gln Leu Asn His Asn Arg Leu His Thr Leu Ala Glu Gly Thr  
155 160 165

Phe Thr Pro Leu Thr Ala Leu Ser His Leu Gln Ile Asn Glu Asn  
170 175 180

Pro Phe Asp Cys Thr Cys Gly Ile Val Trp Leu Lys Thr Trp Ala  
185 190 195

Leu Thr Thr Ala Val Ser Ile Pro Glu Gln Asp Asn Ile Ala Cys  
200 205 210

Thr Ser Pro His Val Leu Lys Gly Thr Pro Leu Ser Arg Leu Pro  
215 220 225

Pro Leu Pro Cys Ser Ala Pro Ser Val Gln Leu Ser Tyr Gln Pro  
230 235 240

Ser Gln Asp Gly Ala Glu Leu Arg Pro Gly Phe Val Leu Ala Leu  
245 250 255

His Cys Asp Val Asp Gly Gln Pro Ala Pro Gln Leu His Trp His  
260 265 270

Ile Gln Ile Pro Ser Gly Ile Val Glu Ile Thr Ser Pro Asn Val  
275 280 285

Gly Thr Asp Gly Arg Ala Leu Pro Gly Thr Pro Val Ala Ser Ser  
290 295 300

Gln Pro Arg Phe Gln Ala Phe Ala Asn Gly Ser Leu Leu Ile Pro  
305 310 315

Asp Phe Gly Lys Leu Glu Glu Gly Thr Tyr Ser Cys Leu Ala Thr  
320 325 330

Asn Glu Leu Gly Ser Ala Glu Ser Ser Val Asp Val Ala Leu Ala  
335 340 345

Thr Pro Gly Glu Gly Glu Asp Thr Leu Gly Arg Arg Phe His  
350 355 360

Gly Lys Ala Val Glu Gly Lys Gly Cys Tyr Thr Val Asp Asn Glu  
365 370 375

Val Gln Pro Ser Gly Pro Glu Asp Asn Val Val Ile Ile Tyr Leu  
380 385 390

Ser Arg Ala Gly Asn Pro Glu Ala Ala Val Ala Glu Gly Val Pro  
395 400 405

Gly Gln Leu Pro Pro Gly Leu Leu Leu Leu Gly Gln Ser Leu Leu  
410 415 420

Leu Phe Phe Phe Leu Thr Ser Phe  
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<210> 18  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 18  
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<210> 19  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 19  
ccaatgtgtg caagcggttg tg 22

<210> 20  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 20  
tcaagagcct ggacctcagc cacaatctca tctctgactt tgccctggagc 50

<210> 21  
<211> 2033  
<212> DNA  
<213> Homo Sapien

<400> 21  
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tgccgcacga ggagtttcc cggcagcggag gaggtcctga gcagcatggc 150  
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tgtgcctgct ggcactgegg gcggaggccg ggccgcgcga ggaggagagc 250  
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agaagatatac ctgattttt cagagggaa aatggcacct ttacacatg 350  
atttcagaaa agcgcaacag agaatgccag ctattcctgt caatatccat 400  
tccatgaatt ttacctggca agctgcaggg caggcagaat acttctatga 450  
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atatattcta aacacaatga aatagggaat ataatgtatg aacttttgc 1900  
atggcttga agcaatataa tatattgtaa acaaaacaca gctcttacct 1950  
aataaacatt ttatactgtt tgtatgtata aaataaaggt gctgctttag 2000  
tttttggaa aaaaaaaaaa aaaaaaaaaa aaa 2033

<210> 22  
<211> 379  
<212> PRT  
<213> Homo Sapien

<400> 22  
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Ser Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly Pro  
20 25 30  
Pro Gln Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala  
35 40 45  
Arg Val Leu Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu  
50 55 60

Gly Lys Met Ala Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln  
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 Arg Met Pro Ala Ile Pro Val Asn Ile His Ser Met Asn Phe Thr  
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 Trp Gln Ala Ala Gly Gln Ala Glu Tyr Phe Tyr Glu Phe Leu Ser  
                   95                    100                  105  
 Leu Arg Ser Leu Asp Lys Gly Ile Met Ala Asp Pro Thr Val Asn  
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 Val Pro Leu Leu Gly Thr Val Pro His Lys Ala Ser Val Val Gln  
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 Val Gly Phe Pro Cys Leu Gly Lys Gln Asp Gly Val Ala Ala Phe  
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 Glu Val Asp Val Ile Val Met Asn Ser Glu Gly Asn Thr Ile Leu  
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 Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr Cys Gln Gln Ala  
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 Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys Asn Glu Arg  
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 Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His Cys Glu  
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 Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys Val  
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 Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn  
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 Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr  
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 Cys Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly  
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 Glu Gln Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly  
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 Gly Lys Cys Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr  
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 Gln Gly Asp Leu Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly  
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 Ala His Gly Thr Cys His Glu Pro Asn Lys Cys Gln Cys Gln Glu  
                   320                    325                  330  
 Gly Trp His Gly Arg His Cys Asn Lys Arg Tyr Glu Ala Ser Leu  
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 Ile His Ala Leu Arg Pro Ala Gly Ala Gln Leu Arg Gln His Thr

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Asn Tyr Ile Trp

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<211> 783

<212> DNA

<213> Homo Sapien

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ctggaattga ggctgagcca aagaccccag ggccgtctca gtctcataaaa 200

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tggggagcct gcggaatctt ttctgaaggc tacatggacc cgctggggag 650

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aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaa 783

<210> 24

<211> 94

<212> PRT

<213> Homo Sapien

<400> 24

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35 40 45  
Trp Val Arg Ser Tyr Glu Phe Thr Ser Asn Ser Cys Ser Gln Arg  
50 55 60  
Ala Val Ile Phe Thr Thr Lys Arg Gly Lys Lys Val Cys Thr His  
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<212> PRT  
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35 40 45  
Ala Val Leu Leu Pro Val Arg Val Asp Ser Ala Thr Ile Pro Arg  
50 55 60  
Gln Asp Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg  
65 70 75  
Arg Ser Leu Lys Glu Glu Glu Cys Pro Ala Gly Ser His Arg Ser  
80 85 90  
Glu Tyr Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr  
95 100 105  
Thr Ile Ala Ser Asn Asn Leu Pro Ser Cys Leu Leu Cys Thr Val  
110 115 120  
Cys Lys Ser Gly Gln Thr Asn Lys Ser Ser Cys Thr Thr Thr Arg  
125 130 135  
Asp Thr Val Cys Gln Cys Glu Lys Gly Ser Phe Gln Asp Lys Asn

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155	160	165
Met Val Lys Val Ser Asn Cys Thr Pro Arg Ser Asp Ile Lys Cys		
170	175	180
Lys Asn Glu Ser Ala Ala Ser Ser Thr Gly Lys Thr Pro Ala Ala		
185	190	195
Glu Glu Thr Val Thr Thr Ile Leu Gly Met Leu Ala Ser Pro Tyr		
200	205	210
His Tyr Leu Ile Ile Val Val Leu Val Ile Ile Leu Ala Val		
215	220	225
Val Val Val Gly Phe Ser Cys Arg Lys Lys Phe Ile Ser Tyr Leu		
230	235	240
Lys Gly Ile Cys Ser Gly Gly Gly Pro Glu Arg Val His		
245	250	255
Arg Val Leu Phe Arg Arg Arg Ser Cys Pro Ser Arg Val Pro Gly		
260	265	270
Ala Glu Asp Asn Ala Arg Asn Glu Thr Leu Ser Asn Arg Tyr Leu		
275	280	285
Gln Pro Thr Gln Val Ser Glu Gln Glu Ile Gln Gly Gln Glu Leu		
290	295	300
Ala Glu Leu Thr Gly Val Thr Val Glu Ser Pro Glu Glu Pro Gln		
305	310	315
Arg Leu Leu Glu Gln Ala Glu Ala Glu Gly Cys Gln Arg Arg Arg		
320	325	330
Leu Leu Val Pro Val Asn Asp Ala Asp Ser Ala Asp Ile Ser Thr		
335	340	345
Leu Leu Asp Ala Ser Ala Thr Leu Glu Glu Gly His Ala Lys Glu		
350	355	360
Thr Ile Gln Asp Gln Leu Val Gly Ser Glu Lys Leu Phe Tyr Glu		
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Glu Asp Glu Ala Gly Ser Ala Thr Ser Cys Leu		
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<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 31  
 <211> 963  
 <212> DNA  
 <213> Homo Sapien

<400> 31  
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 agagctcatt ccagatgcac ccctgtccag tgctgcctat agcatccgca 150  
 gcatcgaaaa gaggcctgtc ctcaaagctc cagccccaa aaggcaaaaa 200  
 tgtgaccact ggactccctg cccatctgac acctatgcct acaggttact 250  
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 attgtcaact atgtaactgg gaatgtgaca gcaacacgat gtttgatata 400  
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 ccaacagccc atatttgcgt agtattttgg gtttgttgc aaccaatgaa 850  
 catttgctag ttgttatcaaa tcttggtagc cagttttt ataccagtat 900  
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 cttaaaaaaaaaaaa aaa 963

<210> 32  
 <211> 235  
 <212> PRT  
 <213> Homo Sapien

<400> 32  
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 1 5 10 15

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Leu	Ile	Pro	Asp	Ala	Pro	Leu	Ser	Ser	Ala	Ala	Tyr	Ser	Ile	Arg
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Ser	Ile	Gly	Glu	Arg	Pro	Val	Leu	Lys	Ala	Pro	Val	Pro	Lys	Arg
						50				55				60
Gln	Lys	Cys	Asp	His	Trp	Thr	Pro	Cys	Pro	Ser	Asp	Thr	Tyr	Ala
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Tyr	Arg	Leu	Leu	Ser	Gly	Gly	Arg	Ser	Lys	Tyr	Ala	Lys	Ile	
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Cys	Phe	Glu	Asp	Asn	Leu	Leu	Met	Gly	Glu	Gln	Leu	Gly	Asn	Val
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Ala	Arg	Gly	Ile	Asn	Ile	Ala	Ile	Val	Asn	Tyr	Val	Thr	Gly	Asn
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Gly	Pro	Met	Thr	Lys	Phe	Ile	Gln	Ser	Ala	Ala	Pro	Lys	Ser	Leu
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Asp	Ala	Lys	Asn	Ala	Ile	Glu	Ala	Leu	Gly	Ser	Lys	Glu	Ile	Arg
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Asn	Met	Lys	Phe	Arg	Ser	Ser	Trp	Val	Phe	Ile	Ala	Ala	Lys	Gly
						185				190				195
Leu	Glu	Leu	Pro	Ser	Glu	Ile	Gln	Arg	Glu	Lys	Ile	Asn	His	Ser
						200				205				210
Asp	Ala	Lys	Asn	Asn	Arg	Tyr	Ser	Gly	Trp	Pro	Ala	Glu	Ile	Gln
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<210> 34  
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<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 34  
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<210> 35  
<211> 18  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 35  
aggcttggaa ctcccttc 18

<210> 36  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 36  
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<210> 37  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

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<210> 38  
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<212> DNA  
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cacctccccgg ccgcggctgc cctctgccccg gtttgtccaa gatggagggc 150  
gctccaccgg ggtcgctcgc cctccggctc ctgctgttcg tggcgctacc 200  
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<211> 330  
<212> PRT  
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20 25 30  
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35 40 45  
Asn Val Thr Thr Leu Lys Asp Asp Gly Asp Ile Ser Lys Gln Gln  
50 55 60

Val Val Leu Asn Ile Thr Tyr Glu Ser Gly Gln Val Tyr Val Asn  
                   65                     70                     75  
 Asp Leu Pro Val Asn Ser Gly Val Thr Arg Ile Ser Cys Gln Thr  
                   80                     85                     90  
 Leu Ile Val Lys Asn Glu Asn Leu Glu Asn Leu Glu Glu Lys Glu  
                   95                     100                    105  
 Tyr Phe Gly Ile Val Ser Val Arg Ile Leu Val His Glu Trp Pro  
                   110                    115                    120  
 Met Thr Ser Gly Ser Ser Leu Gln Leu Ile Val Ile Gln Glu Glu  
                   125                    130                    135  
 Val Val Glu Ile Asp Gly Lys Gln Val Gln Gln Lys Asp Val Thr  
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 Glu Ile Asp Ile Leu Val Lys Asn Arg Gly Val Leu Arg His Ser  
                   155                    160                    165  
 Asn Tyr Thr Leu Pro Leu Glu Glu Ser Met Leu Tyr Ser Ile Ser  
                   170                    175                    180  
 Arg Asp Ser Asp Ile Leu Phe Thr Leu Pro Asn Leu Ser Lys Lys  
                   185                    190                    195  
 Glu Ser Val Ser Ser Leu Gln Thr Thr Ser Gln Tyr Leu Ile Arg  
                   200                    205                    210  
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 Pro Glu Thr Pro Leu Arg Ala Glu Pro Pro Ser Ser Tyr Lys Val  
                   230                    235                    240  
 Met Cys Gln Trp Met Glu Lys Phe Arg Lys Asp Leu Cys Arg Phe  
                   245                    250                    255  
 Trp Ser Asn Val Phe Pro Val Phe Phe Gln Phe Leu Asn Ile Met  
                   260                    265                    270  
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                   275                    280                    285  
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 Lys Val Asp Val Ile Pro Val Thr Ala Ile Asn Leu Tyr Pro Asp  
                   305                    310                    315  
 Gly Pro Glu Lys Arg Ala Glu Asn Leu Glu Asp Lys Thr Cys Ile  
                   320                    325                    330

<210> 40  
 <211> 2498  
 <212> DNA  
 <213> Homo Sapien

<400> 40  
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tcggggaaacc ccgcgcggc tgggtttgc tggctccagc agggccagga 150  
ggccacactgc agcctggtgc tccagactga tgtcacccgg gccgagtgct 200  
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caaagattcg tgcgacggcg tggagtgcgg cccgggcaag gcgtgcccga 350  
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ccggcgccgc tgcaggctcg cggctcagac ggccacccact accgcgacga 450  
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tgtaccgggg ccgctgcgc aagtctgtg agcacgtggt gtgcccgcgg 550  
ccacagtcgt gcgtcgtgga ccagacgggc agcgccact gcgtggtgtg 600  
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<210> 41  
<211> 263  
<212> PRT  
<213> Homo Sapien

<400> 41  
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Ala Leu Ala Trp Ala Val Gly Phe Val Ser Ser Met Gly Ser Gly  
20 25 30  
Asn Pro Ala Pro Gly Gly Val Cys Trp Leu Gln Gln Gly Gln Glu  
35 40 45  
Ala Thr Cys Ser Leu Val Leu Gln Thr Asp Val Thr Arg Ala Glu

50	55	60
Cys Cys Ala Ser Gly Asn Ile Asp Thr Ala Trp Ser Asn Leu Thr		
65	70	75
His Pro Gly Asn Lys Ile Asn Leu Leu Gly Phe Leu Gly Leu Val		
80	85	90
His Cys Leu Pro Cys Lys Asp Ser Cys Asp Gly Val Glu Cys Gly		
95	100	105
Pro Gly Lys Ala Cys Arg Met Leu Gly Gly Arg Pro Arg Cys Glu		
110	115	120
Cys Ala Pro Asp Cys Ser Gly Leu Pro Ala Arg Leu Gln Val Cys		
125	130	135
Gly Ser Asp Gly Ala Thr Tyr Arg Asp Glu Cys Glu Leu Arg Ala		
140	145	150
Ala Arg Cys Arg Gly His Pro Asp Leu Ser Val Met Tyr Arg Gly		
155	160	165
Arg Cys Arg Lys Ser Cys Glu His Val Val Cys Pro Arg Pro Gln		
170	175	180
Ser Cys Val Val Asp Gln Thr Gly Ser Ala His Cys Val Val Cys		
185	190	195
Arg Ala Ala Pro Cys Pro Val Pro Ser Ser Pro Gly Gln Glu Leu		
200	205	210
Cys Gly Asn Asn Asn Val Thr Tyr Ile Ser Ser Cys His Met Arg		
215	220	225
Gln Ala Thr Cys Phe Leu Gly Arg Ser Ile Gly Val Arg His Ala		
230	235	240
Gly Ser Cys Ala Gly Thr Pro Glu Glu Pro Pro Gly Gly Glu Ser		
245	250	255
Ala Glu Glu Glu Glu Asn Phe Val		
260		

<210> 42  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 42  
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<210> 43  
 <211> 18  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 43  
gggtggata gacctgct 18

<210> 44  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 44  
aaggccaaga aggctgcc 18

<210> 45  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 45  
ccaggcctgc agacccag 18

<210> 46  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 46  
cttcctcagt cttccagga tatac 24

<210> 47  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 47  
aagctggata tcctccgtgt tgta 24

<210> 48  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 48  
cctgaagagg catgactgct tttctca 27

<210> 49  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 49  
ggggataaac ctattaatta ttgctac 27

<210> 50  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 50  
aacgtcacct acatctcctc gtgccacatg cgccaggcca cctg 44

<210> 51  
<211> 1690  
<212> DNA  
<213> Homo Sapien

<400> 51  
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gccgagctgc gtgctccgccc agataaaaatc gcgattattt gagccggaat 150  
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gcttaatcga acacttcttg aaaccttgca aaaggccggc ttttctgaga 650

N D E P G M J L S D

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gaggagaaaa caaagaccaa gtacacagga aatccaacaa agatgtatga 900  
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aacatttgate ctccaattga ggaattccat caatattatc aacatatagt 1050  
gacaacttta gttaaggggg aattgaatac atctatctt agctctagac 1100  
ccatagataa atttggcctt aatacagttt taaccactga taattcagat 1150  
ttgttcatta acagtattgg gattgtgccc tctgtgagag aaaaggaaga 1200  
tcctgagcca tcaacagatg gaacatatgt ttggaagatc tttcccaag 1250  
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gctgtgaaga agccatggct tgcataatcct cactataagc ccccgagaa 1350  
atgcccctct atcattctcc atgatcgact ttattacctc aatggcatag 1400  
agtgtgcago aagtgcacatg gagatgagtg ccattgcagc ccacaacgct 1450  
gcactccttg cctatcaccg ctggaacggg cacacagaca tgattgatca 1500  
ggatggctta tatgagaaac ttaaaactga actatgaagt gacacactcc 1550  
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ataaaaagtaa tccctgctgg tcataggaaa aaaaaaaaaa 1690

<210> 52

<211> 505

<212> PRT

<213> Homo Sapien

<400> 52

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Trp	Leu	Leu	Leu	Cys	Ser	Cys	Gly	Cys	Pro	Glu	Gly	Ala	Glu	Leu
			20					25					30	

Arg	Ala	Pro	Pro	Asp	Lys	Ile	Ala	Ile	Ile	Gly	Ala	Gly	Ile	Gly
			35					40					45	

Gly Thr Ser Ala Ala Tyr Tyr Leu Arg Gln Lys Phe Gly Lys Asp

50	55	60
Val Lys Ile Asp Leu Phe Glu Arg Glu	Glu Val Gly Gly Arg	Leu
65	70	75
Ala Thr Met Met Val Gln Gly Gln	Glu Tyr Glu Ala Gly Gly	Ser
80	85	90
Val Ile His Pro Leu Asn Leu His Met	Lys Arg Phe Val Lys Asp	
95	100	105
Leu Gly Leu Ser Ala Val Gln Ala Ser	Gly Gly Leu Leu Gly Ile	
110	115	120
Tyr Asn Gly Glu Thr Leu Val Phe Glu	Glu Ser Asn Trp Phe Ile	
125	130	135
Ile Asn Val Ile Lys Leu Val Trp Arg	Tyr Gly Phe Gln Ser Leu	
140	145	150
Arg Met His Met Trp Val Glu Asp Val	Leu Asp Lys Phe Met Arg	
155	160	165
Ile Tyr Arg Tyr Gln Ser His Asp Tyr	Ala Phe Ser Ser Val Glu	
170	175	180
Lys Leu Leu His Ala Leu Gly Gly Asp	Asp Phe Leu Gly Met Leu	
185	190	195
Asn Arg Thr Leu Leu Glu Thr Leu Gln	Lys Ala Gly Phe Ser Glu	
200	205	210
Lys Phe Leu Asn Glu Met Ile Ala Pro	Val Met Arg Val Asn Tyr	
215	220	225
Gly Gln Ser Thr Asp Ile Asn Ala Phe	Val Gly Ala Val Ser Leu	
230	235	240
Ser Cys Ser Asp Ser Gly Leu Trp Ala	Val Glu Gly Gly Asn Lys	
245	250	255
Leu Val Cys Ser Gly Leu Leu Gln Ala	Ser Lys Ser Asn Leu Ile	
260	265	270
Ser Gly Ser Val Met Tyr Ile Glu Glu	Lys Thr Lys Thr Lys Tyr	
275	280	285
Thr Gly Asn Pro Thr Lys Met Tyr Glu	Val Val Tyr Gln Ile Gly	
290	295	300
Thr Glu Thr Arg Ser Asp Phe Tyr Asp	Ile Val Leu Val Ala Thr	
305	310	315
Pro Leu Asn Arg Lys Met Ser Asn Ile	Thr Phe Leu Asn Phe Asp	
320	325	330
Pro Pro Ile Glu Glu Phe His Gln Tyr	Tyr Gln His Ile Val Thr	
335	340	345

Thr Leu Val Lys Gly Glu Leu Asn Thr Ser Ile Phe Ser Ser Arg  
 350 355 360  
 Pro Ile Asp Lys Phe Gly Leu Asn Thr Val Leu Thr Thr Asp Asn  
 365 370 375  
 Ser Asp Leu Phe Ile Asn Ser Ile Gly Ile Val Pro Ser Val Arg  
 380 385 390  
 Glu Lys Glu Asp Pro Glu Pro Ser Thr Asp Gly Thr Tyr Val Trp  
 395 400 405  
 Lys Ile Phe Ser Gln Glu Thr Leu Thr Lys Ala Gln Ile Leu Lys  
 410 415 420  
 Leu Phe Leu Ser Tyr Asp Tyr Ala Val Lys Lys Pro Trp Leu Ala  
 425 430 435  
 Tyr Pro His Tyr Lys Pro Pro Glu Lys Cys Pro Ser Ile Ile Leu  
 440 445 450  
 His Asp Arg Leu Tyr Tyr Leu Asn Gly Ile Glu Cys Ala Ala Ser  
 455 460 465  
 Ala Met Glu Met Ser Ala Ile Ala Ala His Asn Ala Ala Leu Leu  
 470 475 480  
 Ala Tyr His Arg Trp Asn Gly His Thr Asp Met Ile Asp Gln Asp  
 485 490 495  
 Gly Leu Tyr Glu Lys Leu Lys Thr Glu Leu  
 500 505

<210> 53  
 <211> 728  
 <212> DNA  
 <213> Homo Sapien

<400> 53  
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 cagtttcttc caaccttgcc attgcaataa aaaaggaaaa gaggcctcct 150  
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<210> 54  
<211> 166  
<212> PRT  
<213> Homo Sapien

<400> 54  
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Val Ser Ser Asn Leu Ala Ile Ala Ile Lys Lys Glu Lys Arg Pro  
20 25 30  
Pro Gln Thr Leu Ser Arg Gly Trp Gly Asp Asp Ile Thr Trp Val  
35 40 45  
Gln Thr Tyr Glu Glu Gly Leu Phe Tyr Ala Gln Lys Ser Lys Lys  
50 55 60  
Pro Leu Met Val Ile His His Leu Glu Asp Cys Gln Tyr Ser Gln  
65 70 75  
Ala Leu Lys Lys Val Phe Ala Gln Asn Glu Glu Ile Gln Glu Met  
80 85 90  
Ala Gln Asn Lys Phe Ile Met Leu Asn Leu Met His Glu Thr Thr  
95 100 105  
Asp Lys Asn Leu Ser Pro Asp Gly Gln Tyr Val Pro Arg Ile Met  
110 115 120  
Phe Val Asp Pro Ser Leu Thr Val Arg Ala Asp Ile Ala Gly Arg  
125 130 135  
Tyr Ser Asn Arg Leu Tyr Thr Tyr Glu Pro Arg Asp Leu Pro Leu  
140 145 150  
Leu Ile Glu Asn Met Lys Lys Ala Leu Arg Leu Ile Gln Ser Glu  
155 160 165

Leu

<210> 55  
<211> 537  
<212> DNA  
<213> Homo Sapien

<400> 55

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agaccaggaa cgagaaaaaa gaagtatcag tgacagcgat gaattagctt 200  
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ggataagtca cgataaaacct ggtcacctga aattgaaatt gagccacttc 400  
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acatgaaagc aaagattttg gtttcttaat ttccaca 537

<210> 56  
<211> 85  
<212> PRT  
<213> Homo Sapien

<400> 56  
Met Lys Val Leu Leu Ile Thr Ala Ile Leu Ala Val Ala  
1 5 10 15  
Val Gly Phe Pro Val Ser Gln Asp Gln Glu Arg Glu Lys Arg Ser  
20 25 30  
Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly Phe Phe Val Phe Pro  
35 40 45  
Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg  
50 55 60  
Phe Pro Trp Phe Arg Arg Asn Phe Pro Ile Pro Ile Pro Glu Ser  
65 70 75  
Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys  
80 85

<210> 57  
<211> 2997  
<212> DNA  
<213> Homo Sapien

<400> 57  
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gctcggcctg gccccggcgccg ccggggggagc gccggggcccc gacggtttag 150

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aagaagatct gtatttgcaa ctatggattt gtagggAACG ggaggactca 250  
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aggaccccg aagtgtgcct agccctgtac ccaggcacca actacaccgt 1150  
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atactaatac gaaaatatac tagcctggcc atgccaataa gtttccctgct 2900  
gtgtctgtta ggcagcattt ctttgatgca atttctatttgc tcctatata 2950  
tcaaaagtaa tgtctacatt ccagtaaaaa tatcccgtaa ttaaaaaa 2997

<210> 58  
<211> 747

<212> PRT

<213> Homo Sapien

<400> 58

Met	Gly	Arg	Gly	Pro	Trp	Asp	Ala	Gly	Pro	Ser	Arg	Arg	Leu	Leu
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Pro	Leu	Leu	Leu	Leu	Gly	Leu	Ala	Arg	Gly	Ala	Ala	Gly	Ala	
					20			25				30		
Pro	Gly	Pro	Asp	Gly	Leu	Asp	Val	Cys	Ala	Thr	Cys	His	Glu	His
				35				40				45		
Ala	Thr	Cys	Gln	Gln	Arg	Glu	Gly	Lys	Lys	Ile	Cys	Ile	Cys	Asn
				50				55				60		
Tyr	Gly	Phe	Val	Gly	Asn	Gly	Arg	Thr	Gln	Cys	Val	Asp	Lys	Asn
				65				70				75		
Glu	Cys	Gln	Phe	Gly	Ala	Thr	Leu	Val	Cys	Gly	Asn	His	Thr	Ser
				80				85				90		
Cys	His	Asn	Thr	Pro	Gly	Gly	Phe	Tyr	Cys	Ile	Cys	Leu	Glu	Gly
				95					100				105	
Tyr	Arg	Ala	Thr	Asn	Asn	Asn	Lys	Thr	Phe	Ile	Pro	Asn	Asp	Gly
				110				115				120		
Thr	Phe	Cys	Thr	Asp	Ile	Asp	Glu	Cys	Glu	Val	Ser	Gly	Leu	Cys
				125				130				135		
Arg	His	Gly	Gly	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Phe	Glu	Cys
				140				145				150		
Tyr	Cys	Met	Asp	Gly	Tyr	Leu	Pro	Arg	Asn	Gly	Pro	Glu	Pro	Phe
				155				160				165		
His	Pro	Thr	Thr	Asp	Ala	Thr	Ser	Cys	Thr	Glu	Ile	Asp	Cys	Gly
				170				175				180		
Thr	Pro	Pro	Glu	Val	Pro	Asp	Gly	Tyr	Ile	Ile	Gly	Asn	Tyr	Thr
				185				190				195		
Ser	Ser	Leu	Gly	Ser	Gln	Val	Arg	Tyr	Ala	Cys	Arg	Glu	Gly	Phe
				200				205				210		
Phe	Ser	Val	Pro	Glu	Asp	Thr	Val	Ser	Ser	Cys	Thr	Gly	Leu	Gly
				215				220				225		
Thr	Trp	Glu	Ser	Pro	Lys	Leu	His	Cys	Gln	Glu	Ile	Asn	Cys	Gly
				230				235				240		
Asn	Pro	Pro	Glu	Met	Arg	His	Ala	Ile	Leu	Val	Gly	Asn	His	Ser
				245				250				255		
Ser	Arg	Leu	Gly	Gly	Val	Ala	Arg	Tyr	Val	Cys	Gln	Glu	Gly	Phe
				260				265				270		

Glu Ser Pro Gly Gly Lys Ile Thr Ser Val Cys Thr Glu Lys Gly  
                   275                  280                  285  
 Thr Trp Arg Glu Ser Thr Leu Thr Cys Thr Glu Ile Leu Thr Lys  
                   290                  295                  300  
 Ile Asn Asp Val Ser Leu Phe Asn Asp Thr Cys Val Arg Trp Gln  
                   305                  310                  315  
 Ile Asn Ser Arg Arg Ile Asn Pro Lys Ile Ser Tyr Val Ile Ser  
                   320                  325                  330  
 Ile Lys Gly Gln Arg Leu Asp Pro Met Glu Ser Val Arg Glu Glu  
                   335                  340                  345  
 Thr Val Asn Leu Thr Thr Asp Ser Arg Thr Pro Glu Val Cys Leu  
                   350                  355                  360  
 Ala Leu Tyr Pro Gly Thr Asn Tyr Thr Val Asn Ile Ser Thr Ala  
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 Pro Pro Arg Arg Ser Met Pro Ala Val Ile Gly Phe Gln Thr Ala  
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 Glu Val Asp Leu Leu Glu Asp Asp Gly Ser Phe Asn Ile Ser Ile  
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 Phe Asn Glu Thr Cys Leu Lys Leu Asn Arg Arg Ser Arg Lys Val  
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 Gly Ser Glu His Met Tyr Gln Phe Thr Val Leu Gly Gln Arg Trp  
                   425                  430                  435  
 Tyr Leu Ala Asn Phe Ser His Ala Thr Ser Phe Asn Phe Thr Thr  
                   440                  445                  450  
 Arg Glu Gln Val Pro Val Val Cys Leu Asp Leu Tyr Pro Thr Thr  
                   455                  460                  465  
 Asp Tyr Thr Val Asn Val Thr Leu Leu Arg Ser Pro Lys Arg His  
                   470                  475                  480  
 Ser Val Gln Ile Thr Ile Ala Thr Pro Pro Ala Val Lys Gln Thr  
                   485                  490                  495  
 Ile Ser Asn Ile Ser Gly Phe Asn Glu Thr Cys Leu Arg Trp Arg  
                   500                  505                  510  
 Ser Ile Lys Thr Ala Asp Met Glu Glu Met Tyr Leu Phe His Ile  
                   515                  520                  525  
 Trp Gly Gln Arg Trp Tyr Gln Lys Glu Phe Ala Gln Glu Met Thr  
                   530                  535                  540  
 Phe Asn Ile Ser Ser Ser Arg Asp Pro Glu Val Cys Leu Asp  
                   545                  550                  555  
 Leu Arg Pro Gly Thr Asn Tyr Asn Val Ser Leu Arg Ala Leu Ser

560	565	570
Ser Glu Leu Pro Val Val Ile Ser Leu Thr Thr Gln Ile Thr Glu 575	580	585
Pro Pro Leu Pro Glu Val Glu Phe Phe Thr Val His Arg Gly Pro 590	595	600
Leu Pro Arg Leu Arg Leu Arg Lys Ala Lys Glu Lys Asn Gly Pro 605	610	615
Ile Ser Ser Tyr Gln Val Leu Val Leu Pro Leu Ala Leu Gln Ser 620	625	630
Thr Phe Ser Cys Asp Ser Glu Gly Ala Ser Ser Phe Phe Ser Asn 635	640	645
Ala Ser Asp Ala Asp Gly Tyr Val Ala Ala Glu Leu Leu Ala Lys 650	655	660
Asp Val Pro Asp Asp Ala Met Glu Ile Pro Ile Gly Asp Arg Leu 665	670	675
Tyr Tyr Gly Glu Tyr Tyr Asn Ala Pro Leu Lys Arg Gly Ser Asp 680	685	690
Tyr Cys Ile Ile Leu Arg Ile Thr Ser Glu Trp Asn Lys Val Arg 695	700	705
Arg His Ser Cys Ala Val Trp Ala Gln Val Lys Asp Ser Ser Leu 710	715	720
Met Leu Leu Gln Met Ala Gly Val Gly Leu Gly Ser Leu Ala Val 725	730	735
Val Ile Ile Leu Thr Phe Leu Ser Phe Ser Ala Val 740	745	

<210> 59  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 59  
ccacttgcca tgaacatgcc ac 22

<210> 60  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 60

cctcttgaca gacatagcga gccac 25  
<210> 61  
<211> 43  
<212> DNA  
<213> Artificial Sequence  
  
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<223> Synthetic oligonucleotide probe  
  
<400> 61  
cactcttgc tggggaaacc acacatcttg ccacaactgt ggc 43  
  
<210> 62  
<211> 2015  
<212> DNA  
<213> Homo Sapien  
  
<400> 62  
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ctgctggag gttggggctct ctggagctc tgcaggcccc agcacccgca 150  
gagcagacac tgcgatgaca acggacgaca cagaagtgcc cgctatgact 200  
ctagcaccgg gccacgccc tctggaaact caaacgctga gcgctgagac 250  
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ggggagccaa gagaatttcc cctgcaagag agaccaggag tttcacaaaa 350  
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caccacagag tcagctgcac ctcatgccac ggttgggacc ccactcccc 1050  
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ccagcaggga ccctttctt cttctccctc cgactacaac caacagcagc 1400  
cgagggacga acagcacctt agccaagatc acaacctcag cgaagaccac 1450  
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cagcagctcc accgggaact ccacgcccac gcgcctcact tccaggtctc 1650  
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ggcagcatg tccaagcccc taacccaga tgtggcaaca ggaccctcgc 1850  
tcacatccac cggagtgtat gtatggggag gggcttcacc tggtcccaga 1900  
ggtgtccttg gactcacctt ggcacatgtt ctgtgttca gtaaagagag 1950  
acctgatcac ccatctgtgt gcttccatcc tgcattaaaa ttcaactcagt 2000  
gtggcccaaa aaaaa 2015

<210> 63  
<211> 482  
<212> PRT  
<213> Homo Sapien

<400> 63  
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20 25 30  
Arg Ala Asp Thr Ala Met Thr Thr Asp Asp Thr Glu Val Pro Ala  
35 40 45  
Met Thr Leu Ala Pro Gly His Ala Ala Leu Glu Thr Gln Thr Leu

50	55	60
Ser Ala Glu Thr Ser Ser Arg Ala Ser	Thr Pro Ala Gly Pro Ile	
65	70	75
Pro Glu Ala Glu Thr Arg Gly Ala Lys Arg	Ile Ser Pro Ala Arg	
80	85	90
Glu Thr Arg Ser Phe Thr Lys Thr Ser	Pro Asn Phe Met Val Leu	
95	100	105
Ile Ala Thr Ser Val Glu Thr Ser Ala Ala Ser	Gly Ser Pro Glu	
110	115	120
Gly Ala Gly Met Thr Thr Val Gln Thr	Ile Thr Gly Ser Asp Pro	
125	130	135
Glu Glu Ala Ile Phe Asp Thr Leu Cys	Thr Asp Asp Ser Ser Glu	
140	145	150
Glu Ala Lys Thr Leu Thr Met Asp Ile	Leu Thr Leu Ala His Thr	
155	160	165
Ser Thr Glu Ala Lys Gly Leu Ser Ser	Glu Ser Ser Ala Ser Ser	
170	175	180
Asp Gly Pro His Pro Val Ile Thr Pro	Ser Arg Ala Ser Glu Ser	
185	190	195
Ser Ala Ser Ser Asp Gly Pro His Pro Val	Ile Thr Pro Ser Arg	
200	205	210
Ala Ser Glu Ser Ser Ala Ser Ser Asp	Gly Pro His Pro Val Ile	
215	220	225
Thr Pro Ser Trp Ser Pro Gly Ser Asp	Val Thr Leu Leu Ala Glu	
230	235	240
Ala Leu Val Thr Val Thr Asn Ile Glu	Val Ile Asn Cys Ser Ile	
245	250	255
Thr Glu Ile Glu Thr Thr Ser Ser	Ile Pro Gly Ala Ser Asp	
260	265	270
Ile Asp Leu Ile Pro Thr Glu Gly Val	Lys Ala Ser Ser Thr Ser	
275	280	285
Asp Pro Pro Ala Leu Pro Asp Ser Thr	Glu Ala Lys Pro His Ile	
290	295	300
Thr Glu Val Thr Ala Ser Ala Glu Thr	Leu Ser Thr Ala Gly Thr	
305	310	315
Thr Glu Ser Ala Ala Pro His Ala Thr	Val Gly Thr Pro Leu Pro	
320	325	330
Thr Asn Ser Ala Thr Glu Arg Glu Val	Thr Ala Pro Gly Ala Thr	
335	340	345

Thr Leu Ser Gly Ala Leu Val Thr Val Ser Arg Asn Pro Leu Glu  
                   350                  355                  360  
 Glu Thr Ser Ala Leu Ser Val Glu Thr Pro Ser Tyr Val Lys Val  
                   365                  370                  375  
 Ser Gly Ala Ala Pro Val Ser Ile Glu Ala Gly Ser Ala Val Gly  
                   380                  385                  390  
 Lys Thr Thr Ser Phe Ala Gly Ser Ser Ala Ser Ser Tyr Ser Pro  
                   395                  400                  405  
 Ser Glu Ala Ala Leu Lys Asn Phe Thr Pro Ser Glu Thr Pro Thr  
                   410                  415                  420  
 Met Asp Ile Ala Thr Lys Gly Pro Phe Pro Thr Ser Arg Asp Pro  
                   425                  430                  435  
 Leu Pro Ser Val Pro Pro Thr Thr Asn Ser Ser Arg Gly Thr  
                   440                  445                  450  
 Asn Ser Thr Leu Ala Lys Ile Thr Thr Ser Ala Lys Thr Thr Met  
                   455                  460                  465  
 Lys Pro Gln Gln Pro Arg Pro Arg Leu Pro Gly Arg Gly Arg Pro  
                   470                  475                  480  
 Gln Thr

<210> 64  
 <211> 1252  
 <212> DNA  
 <213> Homo Sapien

<400> 64  
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 gccactccag agccatgct tcgtttctt ccagatttgg cttagctt 100  
 cctgttaatt ctggcttgg gccaggcagt ccaatttcaa gaatatgtct 150  
 ttctccaatt tctgggctta gataaggcgc cttcacccaa gaagttccaa 200  
 cctgtgcctt atatcttcaa gaaaatttgc caggatcgcg aggacgcgc 250  
 gaccactggg gtctcccgag acttatgcta cgtaaaggag ctggcggtcc 300  
 gcgggaatgt acttcgctt ctccagacc aaggttctt tctttacccaa 350  
 aagaaaattt cccaagcttc ctcctgcctg cagaagctcc tctactttaa 400  
 cctgtctgcc atcaaagaaa gggAACAGTT gacattggcc cagctgggcc 450  
 tggacttggg gcccaattct tactataacc tgggaccaga gctggaaactg 500  
 gctatgtcc tggttcagga gcctcatgtg tggggccaga ccacccctaa 550



110	115	120
Gln Leu Thr Leu Ala Gln Leu Gly	Leu Asp Leu Gly Pro Asn Ser	
125	130	135
Tyr Tyr Asn Leu Gly Pro Glu Leu Glu	Leu Ala Leu Phe Leu Val	
140	145	150
Gln Glu Pro His Val Trp Gly Gln Thr	Thr Pro Lys Pro Gly Lys	
155	160	165
Met Phe Val Leu Arg Ser Val Pro Trp	Pro Gln Gly Ala Val His	
170	175	180
Phe Asn Leu Leu Asp Val Ala Lys Asp	Trp Asn Asp Asn Pro Arg	
185	190	195
Lys Asn Phe Gly Leu Phe Leu Glu Ile	Leu Val Lys Glu Asp Arg	
200	205	210
Asp Ser Gly Val Asn Phe Gln Pro Glu	Asp Thr Cys Ala Arg Leu	
215	220	225
Arg Cys Ser Leu His Ala Ser Leu Leu	Val Val Thr Leu Asn Pro	
230	235	240
Asp Gln Cys His Pro Ser Arg Lys Arg	Arg Ala Ala Ile Pro Val	
245	250	255
Pro Lys Leu Ser Cys Lys Asn Leu Cys	His Arg His Gln Leu Phe	
260	265	270
Ile Asn Phe Arg Asp Leu Gly Trp His	Lys Trp Ile Ile Ala Pro	
275	280	285
Lys Gly Phe Met Ala Asn Tyr Cys His	Gly Glu Cys Pro Phe Ser	
290	295	300
Leu Thr Ile Ser Leu Asn Ser Ser Asn	Tyr Ala Phe Met Gln Ala	
305	310	315
Leu Met His Ala Val Asp Pro Glu Ile	Pro Gln Ala Val Cys Ile	
320	325	330
Pro Thr Lys Leu Ser Pro Ile Ser Met	Leu Tyr Gln Asp Asn Asn	
335	340	345
Asp Asn Val Ile Leu Arg His Tyr Glu	Asp Met Val Val Asp Glu	
350	355	360
Cys Gly Cys Gly		

<210> 66  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 66  
gtctgacagc cactccagag 20

<210> 67  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 67  
tctccaattt ctgggcttag ataaggcgcc ttcaccccaag aagttcc 47

<210> 68  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 68  
gtcccaggtt atagtaagaa ttgg 24

<210> 69  
<211> 20  
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<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 69  
gtgttgcgtt cagtccatg 20

<210> 70  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 70  
gctgtctccc atttccatgc 20

<210> 71  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 71  
cgactaccat gttttataa tgtc 24

<210> 72  
<211> 2849  
<212> DNA  
<213> Homo Sapien

<400> 72  
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ggtcgcagag acctcgaga ccgcgcggg gagacggagg tgctgtgggt 100  
gggggggacc tgtggctgct cgtaccgccc cccaccctcc tcttctgcac 150  
tgccgtcctc cgaaagacct tttccctgc tctgtttct tcaccgagtc 200  
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gaagatgggc tccccgtggac agggactctt gctggcgtac tgccctgctcc 350  
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gaacagcagg agtggggaggg gactgaggag ctgccgtcgc ctccggacca 450  
tgccgagagg gctgaagaac aacatgaaaa atacaggccc agtcaggacc 500  
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ggagaagggt gaccgcggag atcgaggcct ccaaggaaaa tatggcaaaa 650  
caggctcagc aggggcccagg ggcacactg gacccaaagg gcagaaggc 700  
tccatggggg cccctggga ggggtgcaag agccactacg ccgcctttc 750  
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ggcaagtct actgctacgt gcccggcctc tacttcttca gcctcaacgt 900  
gcacacactgg aaccagaagg agacctacat gcacatcatg aagaacgagg 950  
aggaggtggt gatcttggc ggcgcagggtgg ggcgcaggcatc catcatgaa 1000  
agccagagcc tggatgttggc gctgcggagag caggaccagg tgtgggtacg 1050  
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gcattcagtg agacgcctg cacacacaga aagccaaagc gatcggtgct 1300  
cccagatccc gcagcctctg gagagagctg acggcagatg aaatcaccag 1350  
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 gagttgctgt gggcggtccc ggaagcagag cgccacactc gctgcttaag 2800  
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 <210> 73  
 <211> 281  
 <212> PRT  
 <213> Homo Sapien  
  
 <400> 73  
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     20   25   30  
  
 Gln Gly Glu Gln Gln Glu Trp Glu Gly Thr Glu Glu Leu Pro Ser  
     35   40   45  
  
 Pro Pro Asp His Ala Glu Arg Ala Glu Glu Gln His Glu Lys Tyr  
     50   55   60  
  
 Arg Pro Ser Gln Asp Gln Gly Leu Pro Ala Ser Arg Cys Leu Arg  
     65   70   75  
  
 Cys Cys Asp Pro Gly Thr Ser Met Tyr Pro Ala Thr Ala Val Pro  
     80   85   90  
  
 Gln Ile Asn Ile Thr Ile Leu Lys Gly Glu Lys Gly Asp Arg Gly  
     95   100   105  
  
 Asp Arg Gly Leu Gln Gly Lys Tyr Gly Lys Thr Gly Ser Ala Gly  
    110   115   120  
  
 Ala Arg Gly His Thr Gly Pro Lys Gly Gln Lys Gly Ser Met Gly  
    125   130   135  
  
 Ala Pro Gly Glu Arg Cys Lys Ser His Tyr Ala Ala Phe Ser Val  
    140   145   150  
  
 Gly Arg Lys Lys Pro Met His Ser Asn His Tyr Tyr Gln Thr Val  
    155   160   165  
  
 Ile Phe Asp Thr Glu Phe Val Asn Leu Tyr Asp His Phe Asn Met  
    170   175   180  
  
 Phe Thr Gly Lys Phe Tyr Cys Tyr Val Pro Gly Leu Tyr Phe Phe  
    185   190   195  
  
 Ser Leu Asn Val His Thr Trp Asn Gln Lys Glu Thr Tyr Leu His  
    200   205   210  
  
 Ile Met Lys Asn Glu Glu Glu Val Val Ile Leu Phe Ala Gln Val  
    215   220   225  
  
 Gly Asp Arg Ser Ile Met Gln Ser Gln Ser Leu Met Leu Glu Leu

230                    235                    240

Arg Glu Gln Asp Gln Val Trp Val Arg Leu Tyr Lys Gly Glu Arg  
245                    250                    255

Glu Asn Ala Ile Phe Ser Glu Glu Leu Asp Thr Tyr Ile Thr Phe  
260                    265                    270

Ser Gly Tyr Leu Val Lys His Ala Thr Glu Pro  
275                    280

<210> 74  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 74  
 tacaggccca gtcaggacca gggg 24

<210> 75  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 75  
 ctgaagaagt agaggccggg cacg 24

<210> 76  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 76  
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<210> 77  
<211> 1042  
<212> DNA  
<213> Homo Sapien

<400> 77  
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 tcaggccaca gacggacatg gctgctcaag gctggtccat gctcctgctg 150  
 gctgtccta accttaggcat ctgcgtccgtt ccctgtgaca ctcaagagct 200

acgatgtctg tgtattcagg aacactctga attcattcct ctcaaactca 250  
ttaaaaatat aatggtgata ttcgagacca tttactgcaa cagaaaggaa 300  
gtgatagcag tcccaaaaaa tgggagtatg atttgttgg atcctgatgc 350  
tccatgggtg aaggctactg ttggccaat tactaacagg ttcc tacctg 400  
aggacctcaa acaaaaggaa tttccaccgg caatgaagct tctgtatagt 450  
gtttagcatg aaaagcctct atatcttca tttgggagac ctgagaacaa 500  
gagaatattt cccttccaa ttcccggagac ctctagacac tttgctgatt 550  
tagctcacaa cagtgatagg aattttctac gggactccag tgaagtcagc 600  
ttgacaggca gtgatgccta aaagccactc atgaggcaaa gagttcaag 650  
gaagctctcc tcctggagtt ttggcggtct cattcttata ctctattccc 700  
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ccccatcccc atttcttgcatt accatata atggcatcat atacccttt 850  
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tatcccactc cactatggc tgttacagag tgcatctcggttgtagagcaa 950  
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<210> 78  
<211> 167  
<212> PRT  
<213> Homo Sapien

<400> 78  
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Leu Cys Ile Gln Glu His Ser Glu Phe Ile Pro Leu Lys Leu Ile  
35 40 45  
Lys Asn Ile Met Val Ile Phe Glu Thr Ile Tyr Cys Asn Arg Lys  
50 55 60  
Glu Val Ile Ala Val Pro Lys Asn Gly Ser Met Ile Cys Leu Asp  
65 70 75  
Pro Asp Ala Pro Trp Val Lys Ala Thr Val Gly Pro Ile Thr Asn  
80 85 90

Arg Phe Leu Pro Glu Asp Leu Lys Gln Lys Glu Phe Pro Pro Ala  
95 100 105

Met Lys Leu Leu Tyr Ser Val Glu His Glu Lys Pro Leu Tyr Leu  
110 115 120

Ser Phe Gly Arg Pro Glu Asn Lys Arg Ile Phe Pro Phe Pro Ile  
125 130 135

Arg Glu Thr Ser Arg His Phe Ala Asp Leu Ala His Asn Ser Asp  
140 145 150

Arg Asn Phe Leu Arg Asp Ser Ser Glu Val Ser Leu Thr Gly Ser  
155 160 165

Asp Ala

DNA sequence analysis

<210> 79  
<211> 798  
<212> DNA  
<213> Homo Sapien

<220>  
<221> unsure  
<222> 794  
<223> unknown base

<400> 79  
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cctcaagtac agccaaagga agattcccgc caaggttgctc cgcaagctacc 150  
ggaagcagga accaagctta ggctgctcca tcccagctat cctgttcttg 200  
ccccgcaagc gctctcaggc agagctatgt gcagacccaa aggagctctg 250  
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gccccacagca ggccaggatcc agagagaccg aggagggaga gtctcccagg 650  
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accctggacc tgataccggtt ccccaagtaca ccccacctct tccttgtaaa 750



<211> 924  
<212> DNA  
<213> Homo Sapien

<400> 83  
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cggtctcagg agatgtctga tttccacaga catgcaccat atagaagaga 150  
gtttccaaga aatcaaaaga gccatccaag ctaaggacac cttcccaa 200  
gtcactatcc tgtccacatt ggagactctg cagatcatta agcccttaga 250  
tgtgtgctgc gtgaccaaga acctcctggc gttctacgtg gacagggtgt 300  
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ataaaattcca tattttacat atga 924

<210> 84  
<211> 177  
<212> PRT  
<213> Homo Sapien

<400> 84  
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Ser Thr Asp Met His His Ile Glu Glu Ser Phe Gln Glu Ile Lys  
35 40 45

Arg Ala Ile Gln Ala Lys Asp Thr Phe Pro Asn Val Thr Ile Leu  
                   50   60  
 Ser Thr Leu Glu Thr Leu Gln Ile Ile Lys Pro Leu Asp Val Cys  
                   65   70                         75  
 Cys Val Thr Lys Asn Leu Leu Ala Phe Tyr Val Asp Arg Val Phe  
                   80   85                         90  
 Lys Asp His Gln Glu Pro Asn Pro Lys Ile Leu Arg Lys Ile Ser  
                   95   100                         105  
 Ser Ile Ala Asn Ser Phe Leu Tyr Met Gln Lys Thr Leu Arg Gln  
                   110   115                         120  
 Cys Gln Glu Gln Arg Gln Cys His Cys Arg Gln Glu Ala Thr Asn  
                   125   130                         135  
 Ala Thr Arg Val Ile His Asp Asn Tyr Asp Gln Leu Glu Val His  
                   140   145                         150  
 Ala Ala Ala Ile Lys Ser Leu Gly Glu Leu Asp Val Phe Leu Ala  
                   155   160                         165  
 Trp Ile Asn Lys Asn His Glu Val Met Phe Ser Ala  
                   170   175

<210> 85  
 <211> 2137  
 <212> DNA  
 <213> Homo Sapien

<400> 85  
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 tggcggggtt caccgggct gggacaagaa gccgcccgcct gcctgcccgg 150  
 gcccggggag ggggtgggg ctggggccgg aggcggggtg tgagtgggtg 200  
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cagcgtgcgg tacctctgca tggcgccga cggcaagatg caggggctgc 800  
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cagtgc当地 cagcggcagc tgtacaagaa cagaggctt cttccactct 950  
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gaggtttggtt ttgttatatta aaatggagtt tgtttgt 2137

<210> 86

<211> 216

<212> PRT

<213> Homo Sapien

<400> 86

Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly  
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Leu Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala  
20 25 30

Gly Pro His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg  
35 40 45

His Leu Tyr Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu  
50 55 60

Arg Ile Arg Ala Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser  
65 70 75

Ala His Ser Leu Leu Glu Ile Lys Ala Val Ala Leu Arg Thr Val  
80 85 90

Ala Ile Lys Gly Val His Ser Val Arg Tyr Leu Cys Met Gly Ala  
95 100 105

Asp Gly Lys Met Gln Gly Leu Leu Gln Tyr Ser Glu Glu Asp Cys  
110 115 120

Ala Phe Glu Glu Glu Ile Arg Pro Asp Gly Tyr Asn Val Tyr Arg  
125 130 135

Ser Glu Lys His Arg Leu Pro Val Ser Leu Ser Ser Ala Lys Gln  
140 145 150

Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu Pro Leu Ser His Phe  
155 160 165

Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro Glu Asp Leu Arg  
170 175 180

Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu Glu Thr Asp  
185 190 195

Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala Val Arg  
200 205 210

Ser Pro Ser Phe Glu Lys  
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<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 87  
atccgcccag atggctacaa tgtgta 26

<210> 88  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 88  
gcctccccgt ctccctgagc agtgccaaac agcggcagtg ta 42

<210> 89  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 89  
ccagtcccggt gacaagcccc aa 22

<210> 90  
<211> 1857  
<212> DNA  
<213> Homo Sapien

<400> 90  
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gatggggaca aaggcgcaag tcgagaggaa actgttgtgc ctcttcataat 100  
tggcgatcct gttgtgtcc ctggcattgg gcagtgttac agtgcactct 150  
tctgaacctg aagtcaaat tcctgagaat aatcctgtga agttgtcctg 200  
tgcctactcg ggctttctt ctccccgtgt ggagtggaaat tttgaccaag 250  
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acggaaagac actggggacat acacttgtat ggtctctgag gaaggcggca 400  
acagctatgg ggaggtcaag gtcaagctca tcgtgcttgt gcctccatcc 450  
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agctgctcag gagcctggca acaagagcaa aactccagct caaaaaaaaaa 1850  
aaaaaaaa 1857

<210> 91  
<211> 299  
<212> PRT  
<213> Homo Sapien

<400> 91

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Ile Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr  
 20 25 30

Val His Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro  
 35 40 45

Val Lys Leu Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val  
 50 55 60

Glu Trp Lys Phe Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr  
 65 70 75

Asn Asn Lys Ile Thr Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu  
 80 85 90

Pro Thr Gly Ile Thr Phe Lys Ser Val Thr Arg Glu Asp Thr Gly  
 95 100 105

Thr Tyr Thr Cys Met Val Ser Glu Glu Gly Asn Ser Tyr Gly  
 110 115 120

Glu Val Lys Val Lys Leu Ile Val Leu Val Pro Pro Ser Lys Pro  
 125 130 135

Thr Val Asn Ile Pro Ser Ser Ala Thr Ile Gly Asn Arg Ala Val  
 140 145 150

Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro Pro Ser Glu Tyr Thr  
 155 160 165

Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn Pro Lys Ser Thr  
 170 175 180

Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro Thr Thr Gly  
 185 190 195

Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly Glu Tyr  
 200 205 210

Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser Asn  
 215 220 225

Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val  
 230 235 240

Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe  
 245 250 255

Gly Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys  
 260 265 270

Lys Gly Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala  
 275 280 285

Arg Ser Glu Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val

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<210> 92
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 92
tcgcggagct gtgttctgtt tccc 24

<210> 93
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 93
tgatcgcgat ggggacaaag gcgcaagctc gagagggaaac ttttgtgcct 50

<210> 94
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 94
acacctggtt caaagatgg 20

<210> 95
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 95
taggaagagt tgctgaaggc acgg 24

<210> 96
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 96
ttgccttact caggtgctac 20

<210> 97

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<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 97  
actcagcagt ggttagaaag 20

<210> 98  
<211> 1200  
<212> DNA  
<213> Homo Sapien

<400> 98  
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gtgagggacc agggcgccat gaccgaccag ctgagcaggc ggcagatccg 150  
cgagtagccaa ctctacagca ggaccagtgg caagcacgtg caggtcacccg 200  
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cacgcggcag gggcggcccc gccaggcttc ccgcagccgc cagaaccagc 500  
gcgaggcccc cttcatcaag cgcccttacc aaggccagct gcccttcccc 550  
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tcggatctcc ctcagtcgtc ccccgcccc caaactccctc ctggctagac 1050

tgttaggaagg gactttgtt tggggggggg aaagaaaagg 1100  
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<210> 99  
<211> 205  
<212> PRT  
<213> Homo Sapien

<400> 99  
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Ala Met Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln  
35 40 45  
Leu Tyr Ser Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg  
50 55 60  
Arg Ile Ser Ala Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu  
65 70 75  
Ile Val Glu Thr Asp Thr Phe Gly Ser Arg Val Arg Ile Lys Gly  
80 85 90  
Ala Glu Ser Glu Lys Tyr Ile Cys Met Asn Lys Arg Gly Lys Leu  
95 100 105  
Ile Gly Lys Pro Ser Gly Lys Ser Lys Asp Cys Val Phe Thr Glu  
110 115 120  
Ile Val Leu Glu Asn Asn Tyr Thr Ala Phe Gln Asn Ala Arg His  
125 130 135  
Glu Gly Trp Phe Met Ala Phe Thr Arg Gln Gly Arg Pro Arg Gln  
140 145 150  
Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu Ala His Phe Ile Lys  
155 160 165  
Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn His Ala Glu Lys  
170 175 180  
Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr Arg Arg Thr  
185 190 195  
Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr  
200 205

<210> 100  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 100  
cagtacgtga gggaccaggg cgccatga 28

<210> 101  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 101  
ccggtgacct gcacgtgctt gccca 24

<210> 102  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<220>  
<221> unsure  
<222> 21  
<223> unknown base

<400> 102  
gcggatctgc cgcctgctca nctggtcggt catggcgccc t 41

<210> 103  
<211> 1679  
<212> DNA  
<213> Homo Sapien

<400> 103  
gttgtgtcct tcagcaaaac agtggattta aatctccttg cacaagcttg 50  
agagcaacac aatctatcag gaaagaaaaga aagaaaaaaaaa ccgaacctga 100  
caaaaaagaa gaaaaagaag aagaaaaaaaaa atcatgaaaaa ccatccagcc 150  
aaaaatgcac aattctatct cttggcaat ctgcacgggg ctggctgctc 200  
tgtgtctctt ccaaggagtg cccgtgcgca gcggagatgc cacctcccc 250  
aaagctatgg acaacgtgac ggtccggcag ggggagagcgc ccaccctcag 300  
gtgcactatt gacaaccggg tcacccgggt ggcctggcta aaccgcagca 350  
ccatcctcta tgctggaat gacaagtggt gcctggatcc tcgcgtggtc 400  
cttctgagca acacccaaac gcagttacagc atcgagatcc agaacgtgga 450  
tgtgtatgac gagggccctt acacctgctc ggtgcagaca gacaaccacc 500

caaagacctc tagggccac ctcattgtgc aagtatctcc caaaattgta 550  
gagatttctt cagatatctc catatatgaa gggacaata ttagcctcac 600  
ctgcatacgca actggtagac cagagcctac ggtaacttgg agacacatct 650  
ctcccaaagc ggttggctt gtgagtgaag acgaataactt ggaaattcag 700  
ggcatcaccc gggagcagtc agggactac gagtgcagtg cctccaatga 750  
cgtggccgcg cccgtggac ggagagtaaa ggtaaccgtg aactatccac 800  
catacatttc agaagccaag ggtacaggtg tccccgtggg aaaaaagggg 850  
acactgcagt gtgaagcctc agcagtcccc tcagcagaat tccagtggta 900  
caaggatgac aaaagactga ttgaaggaaa gaaaggggtg aaagtggaaa 950  
acagaccttt cctctcaaaa ctcatcttct tcaatgtctc tgaacatgac 1000  
tatgggaact acacttgctg ggcctccaac aagctggcc acaccaatgc 1050  
cagcatcatg ctatggtc caggcgccgt cagcgaggtg agcaacggca 1100  
cgtcgaggag ggcaggctgc gtctggctgc tgccctttct ggtcttgcac 1150  
ctgcttctca aattttgatg tgagtgccac ttccccaccc gggaaaggct 1200  
gccgccacca ccaccaccaa cacaacagca atggcaacac cgacagcaac 1250  
caatcagata tatacaaatg aaattagaag aaacacagcc tcatggaca 1300  
gaaatttgag ggaggggaac aaagaatact ttggggggaa aagagttta 1350  
aaaaagaaaat tgaaaattgc cttgcagata tttaggtaca atggagttt 1400  
ctttcccaa acgggaagaa cacagcacac ccggcttggc cccactgcaa 1450  
gtgcacgt gcaaccttt tggtgccagt gtggcaagg gctcagcctc 1500  
tctgccaca gagtgccccc acgtggaaca ttctggagct ggccatccca 1550  
aattcaatca gtccatagag acgaacagaa tgagaccttc cggcccaagc 1600  
gtggcgctgc gggcactttg gttagactgtg ccaccacggc gtgtgttgtg 1650  
aacgtgaaa taaaaagagc aaaaaaaaaa 1679

<210> 104  
<211> 344  
<212> PRT  
<213> Homo Sapien

<400> 104  
Met Lys Thr Ile Gln Pro Lys Met His Asn Ser Ile Ser Trp Ala  
1 5 10 15  
Ile Phe Thr Gly Leu Ala Ala Leu Cys Leu Phe Gln Gly Val Pro

20	25	30
Val Arg Ser Gly Asp Ala Thr Phe Pro Lys Ala Met Asp Asn Val		
35	40	45
Thr Val Arg Gln Gly Glu Ser Ala Thr Leu Arg Cys Thr Ile Asp		
50	55	60
Asn Arg Val Thr Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu		
65	70	75
Tyr Ala Gly Asn Asp Lys Trp Cys Leu Asp Pro Arg Val Val Leu		
80	85	90
Leu Ser Asn Thr Gln Thr Gln Tyr Ser Ile Glu Ile Gln Asn Val		
95	100	105
Asp Val Tyr Asp Glu Gly Pro Tyr Thr Cys Ser Val Gln Thr Asp		
110	115	120
Asn His Pro Lys Thr Ser Arg Val His Leu Ile Val Gln Val Ser		
125	130	135
Pro Lys Ile Val Glu Ile Ser Ser Asp Ile Ser Ile Asn Glu Gly		
140	145	150
Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr Gly Arg Pro Glu Pro		
155	160	165
Thr Val Thr Trp Arg His Ile Ser Pro Lys Ala Val Gly Phe Val		
170	175	180
Ser Glu Asp Glu Tyr Leu Glu Ile Gln Gly Ile Thr Arg Glu Gln		
185	190	195
Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp Val Ala Ala Pro		
200	205	210
Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro Tyr Ile		
215	220	225
Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly Thr		
230	235	240
Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln Trp		
245	250	255
Tyr Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys Gly Val Lys		
260	265	270
Val Glu Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe Asn Val		
275	280	285
Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys		
290	295	300
Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala		
305	310	315

Val Ser Glu Val Ser Asn Gly Thr Ser Arg Arg Ala Gly Cys Val  
320 325 330

Trp Leu Leu Pro Leu Leu Val Leu His Leu Leu Leu Lys Phe  
335 340

<210> 105

<211> 1734

<212> DNA

<213> Homo Sapien

<400> 105

gtggactctg agaagccag gcagttgagg acaggagaga gaaggctgca 50  
gaccagagg gagggaggac agggagtcgg aaggaggagg acagaggagg 100  
gcacagagac gcagagcaag ggccgcaagg aggagacctt ggtgggagga 150  
agacactctg gagagagagg gggctggca gagatgaagt tccaggggcc 200  
cctggcctgc ctctcgctgg ccctctgcct gggcagtggg gaggctggcc 250  
ccctgcagag cggagaggaa agcactggga caaatattgg ggaggccctt 300  
ggacatggcc tgggagacgc cctgagcgaa ggggtggaa aggccattgg 350  
caaagaggcc ggaggggcag ctggctctaa agtcagttag gcccattggcc 400  
aagggaccag agaagcagtt ggcaactggag tcaggcaggt tccaggcttt 450  
ggcgcagcag atgctttggg caacagggtc ggggaagcag cccatgctct 500  
ggaaaacact gggcacgaga ttggcagaca ggcagaagat gtcattcgac 550  
acggagcaga tgctgtccgc ggctcctggc aggggtgcc tggccacagt 600  
ggtgcttggg aaacttctgg aggccatggc atctttggct ctcaagggtgg 650  
ccttggaggc cagggccagg gcaatcctgg aggtctgggg actccgtggg 700  
tccacggata ccccgaaac tcagcaggca gctttggaaat gaatcctcag 750  
ggagctccct ggggtcaagg aggcaatggc gggccaccaa actttggac 800  
caacactcag ggagctgtgg cccagcctgg ctatggttca gtgagagcca 850  
gcaaccagaa tgaaggggtgc acgaatcccc caccatctgg ctcaggtgg 900  
ggctccagca actctggggg aggcaagcggc tcacagtcgg gcagcagtgg 950  
cagtggcagc aatggtgaca acaacaatgg cagcagcagt ggtggcagca 1000  
gcagtggcag cagcagtggc agcagcagtgc gcggcagcag tggcggcagc 1050  
agtggtgca gcagtggcaa cagtggtgcc agcagaggtg acagcggcag 1100  
tgagtccctcc tggggatcca gcaccggctc ctccctccggc aaccacggtg 1150

ggagcggcgg aggaaaatgga cataaaccgg ggtgtaaaaa gccagggaat 1200  
gaagcccgcg ggagcgggaa atctggatt caggcttca gaggacaggg 1250  
agtttccagc aacatgaggg aaataagcaa agagggcaat cgccctccttg 1300  
gaggctctgg agacaattat cggggcaag ggtcgagctg gggcagtgg 1350  
ggaggtgacg ctgttggtgg agtcaatact gtgaactctg agacgtctcc 1400  
tggatgttt aactttgaca cttctggaa gaattttaaa tccaagctgg 1450  
gtttcatcaa ctgggatgcc ataaacaagg accagagaag ctctcgcatc 1500  
ccgtgacctc cagacaagga gccaccagat tggatggag cccccacact 1550  
ccctccttaa aacaccaccc tctcatcaact aatctcagcc cttgccccttg 1600  
aaataaacct tagctgcccc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1734

<210> 106

<211> 440

<212> PRT

<213> Homo Sapien

<400> 106

Met	Lys	Phe	Gln	Gly	Pro	Leu	Ala	Cys	Leu	Leu	Leu	Ala	Leu	Cys
1					5				10				15	

Leu	Gly	Ser	Gly	Glu	Ala	Gly	Pro	Leu	Gln	Ser	Gly	Glu	Glu	Ser
					20				25				30	

Thr	Gly	Thr	Asn	Ile	Gly	Glu	Ala	Leu	Gly	His	Gly	Leu	Gly	Asp
					35				40				45	

Ala	Leu	Ser	Glu	Gly	Val	Gly	Lys	Ala	Ile	Gly	Lys	Glu	Ala	Gly
					50				55				60	

Gly	Ala	Ala	Gly	Ser	Lys	Val	Ser	Glu	Ala	Leu	Gly	Gln	Gly	Thr
					65				70				75	

Arg	Glu	Ala	Val	Gly	Thr	Gly	Val	Arg	Gln	Val	Pro	Gly	Phe	Gly
					80				85				90	

Ala	Ala	Asp	Ala	Leu	Gly	Asn	Arg	Val	Gly	Glu	Ala	Ala	His	Ala
					95				100				105	

Leu	Gly	Asn	Thr	Gly	His	Glu	Ile	Gly	Arg	Gln	Ala	Glu	Asp	Val
					110				115				120	

Ile	Arg	His	Gly	Ala	Asp	Ala	Val	Arg	Gly	Ser	Trp	Gln	Gly	Val
					125				130				135	

Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile

140	145	150												
Phe	Gly	Ser	Gln	Gly	Gly	Leu	Gly	Gly	Gln	Gly	Gln	Gly	Asn	Pro
			155				160				165			
Gly	Gly	Leu	Gly	Thr	Pro	Trp	Val	His	Gly	Tyr	Pro	Gly	Asn	Ser
		170					175				180			
Ala	Gly	Ser	Phe	Gly	Met	Asn	Pro	Gln	Gly	Ala	Pro	Trp	Gly	Gln
			185				190				195			
Gly	Gly	Asn	Gly	Gly	Pro	Pro	Asn	Phe	Gly	Thr	Asn	Thr	Gln	Gly
			200				205				210			
Ala	Val	Ala	Gln	Pro	Gly	Tyr	Gly	Ser	Val	Arg	Ala	Ser	Asn	Gln
			215				220				225			
Asn	Glu	Gly	Cys	Thr	Asn	Pro	Pro	Pro	Ser	Gly	Ser	Gly	Gly	Gly
			230				235				240			
Ser	Ser	Asn	Ser	Gly	Gly	Ser	Gly	Ser	Gln	Ser	Gly	Ser	Ser	Ser
			245				250				255			
Gly	Ser	Gly	Ser	Asn	Gly	Asp	Asn	Asn	Gly	Ser	Ser	Ser	Gly	
			260				265				270			
Gly	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Gly	Gly	Ser
			275				280				285			
Ser	Gly	Gly	Ser	Ser	Gly	Ser	Ser	Gly	Asn	Ser	Gly	Gly	Ser	
			290				295				300			
Arg	Gly	Asp	Ser	Gly	Ser	Glu	Ser	Ser	Trp	Gly	Ser	Ser	Thr	Gly
			305				310				315			
Ser	Ser	Ser	Gly	Asn	His	Gly	Gly	Ser	Gly	Gly	Asn	Gly	His	
			320				325				330			
Lys	Pro	Gly	Cys	Glu	Lys	Pro	Gly	Asn	Glu	Ala	Arg	Gly	Ser	Gly
			335				340				345			
Glu	Ser	Gly	Ile	Gln	Gly	Phe	Arg	Gly	Gln	Gly	Val	Ser	Ser	Asn
			350				355				360			
Met	Arg	Glu	Ile	Ser	Lys	Glu	Gly	Asn	Arg	Leu	Leu	Gly	Gly	Ser
			365				370				375			
Gly	Asp	Asn	Tyr	Arg	Gly	Gln	Gly	Ser	Ser	Trp	Gly	Ser	Gly	Gly
			380				385				390			
Gly	Asp	Ala	Val	Gly	Gly	Val	Asn	Thr	Val	Asn	Ser	Glu	Thr	Ser
			395				400				405			
Pro	Gly	Met	Phe	Asn	Phe	Asp	Thr	Phe	Trp	Lys	Asn	Phe	Lys	Ser
			410				415				420			
Lys	Leu	Gly	Phe	Ile	Asn	Trp	Asp	Ala	Ile	Asn	Lys	Asp	Gln	Arg
			425				430				435			

Ser Ser Arg Ile Pro  
440

<210> 107  
<211> 918  
<212> DNA  
<213> Homo Sapien

<400> 107  
agccaggcag cacatcacag cgggaggagc tgtcccaggt ggcccagtc 50  
agcaatggca atgggggtcc ccagagtcat tctgctotgc ctcttgggg 100  
ctgcgtctg cctgacaggg tcccaagccc tgcagtgcta cagcttttag 150  
cacacctact ttggccctt tgacctcagg gccatgaagc tgcccagcat 200  
ctccgtcct catgagtgct ttgaggctat cctgtctctg gacaccgggt 250  
atcgcgccgc ggtgaccctg gtgcggaaagg gctgctggac cgggcctcct 300  
gcgggccaga cgcaatcgaa cccggacgcg ctgccccag actactcggt 350  
ggtgccggc tgcacaactg acaaatgcaa cgccccacctc atgactcatg 400  
acgcctccc caacctgagc caagcacccg acccgccgac gtcagcggc 450  
gccgagtgct acgcctgtat cgggtccac caggatgact gcgctatcgg 500  
caggtcccga cgagtccagt gtcaccagga ccagacccgc tgcttccagg 550  
gcagtggcag aatgacagtt ggcaatttct cagtcctgt gtacatcaga 600  
acctgccacc ggccctcctg caccacccg ggcaccacca gcccctggac 650  
agccatcgac ctccagggt cctgctgtga ggggtacctc tgcaacagga 700  
aatccatgac ccagcccttc accagtgctt cagccaccac ccctccccga 750  
gcactacagg tcctggccct gtcctccca gtcctcctgc tggggggct 800  
ctcagcatag accgccccctc caggatgctg gggacagggc tcacacacct 850  
cattcttgct gttcagccc ctatcacata gtcactgga aaatgatgtt 900  
aaagtaagaa ttgcaaaa 918

<210> 108  
<211> 251  
<212> PRT  
<213> Homo Sapien

<400> 108  
Met Ala Met Gly Val Pro Arg Val Ile Leu Leu Cys Leu Phe Gly  
1 5 10 15  
Ala Ala Leu Cys Leu Thr Gly Ser Gln Ala Leu Gln Cys Tyr Ser  
20 25 30

Phe Glu His Thr Tyr Phe Gly Pro Phe Asp Leu Arg Ala Met Lys  
                  35                        40                        45  
 Leu Pro Ser Ile Ser Cys Pro His Glu Cys Phe Glu Ala Ile Leu  
                  50                        55                        60  
 Ser Leu Asp Thr Gly Tyr Arg Ala Pro Val Thr Leu Val Arg Lys  
                  65                        70                        75  
 Gly Cys Trp Thr Gly Pro Pro Ala Gly Gln Thr Gln Ser Asn Pro  
                  80                        85                        90  
 Asp Ala Leu Pro Pro Asp Tyr Ser Val Val Arg Gly Cys Thr Thr  
                  95                        100                       105  
 Asp Lys Cys Asn Ala His Leu Met Thr His Asp Ala Leu Pro Asn  
                  110                       115                       120  
 Leu Ser Gln Ala Pro Asp Pro Pro Thr Leu Ser Gly Ala Glu Cys  
                  125                       130                       135  
 Tyr Ala Cys Ile Gly Val His Gln Asp Asp Cys Ala Ile Gly Arg  
                  140                       145                       150  
 Ser Arg Arg Val Gln Cys His Gln Asp Gln Thr Ala Cys Phe Gln  
                  155                       160                       165  
 Gly Ser Gly Arg Met Thr Val Gly Asn Phe Ser Val Pro Val Tyr  
                  170                       175                       180  
 Ile Arg Thr Cys His Arg Pro Ser Cys Thr Thr Glu Gly Thr Thr  
                  185                       190                       195  
 Ser Pro Trp Thr Ala Ile Asp Leu Gln Gly Ser Cys Cys Glu Gly  
                  200                       205                       210  
 Tyr Leu Cys Asn Arg Lys Ser Met Thr Gln Pro Phe Thr Ser Ala  
                  215                       220                       225  
 Ser Ala Thr Thr Pro Pro Arg Ala Leu Gln Val Leu Ala Leu Leu  
                  230                       235                       240  
 Leu Pro Val Leu Leu Val Gly Leu Ser Ala  
                  245                       250

<210> 109  
 <211> 1813  
 <212> DNA  
 <213> Homo Sapien

<400> 109  
 ggagccgccc tgggtgtcag cggatcggtc cccgcgcacg ctccggccgt 50  
 cgccgcaggct cggcacctgc aggtccgtgc gtccccggc tgccgcacct 100  
 gactccgtcc cggccaggga gggccatgtat ttccctcccg gggccctgg 150  
 tgaccaactt gctgcggttt ttgttcctgg ggctgagtgc octcgcgccc 200

ccctcgcccc cccagctgca actgcacttg cccgccaaacc gggtgcaggc 250  
ggtggaggga ggggaagtgg tgcttccagc gtggcacacc ttgcacgggg 300  
aggtgtcttc atcccagcca tgggaggtgc cctttgtat gtggttcttc 350  
aaacagaaag aaaaggagga tcaggtgttgc tcctacatca atggggtcac 400  
aacaagcaaa cctggagttat ccttggtcta ctccatgccc tcccgaaacc 450  
tgtccctgca gctggagggt ctccaggaga aagactctgg cccctacagc 500  
tgctccgtga atgtgcaaga caaacaaggc aaatcttaggg gccacagcat 550  
caaaaacctta gaactcaatg tactggttcc tccagctcct ccattctgcc 600  
gtctccaggg tgtgccccat gtggggcaa acgtgaccct gagctgccag 650  
tctccaagga gtaagccgc tgtccaatac cagtgggatc ggcagcttcc 700  
atccttccag actttcttg caccaggatt agatgtcatc cgtgggtctt 750  
taaggctcac caaccttgc tcttccatgg ctggagttcta tgtctgcaag 800  
gcccacaatg aggtggcac tgccaatgt aatgtgacgc tggaagttag 850  
cacagggcct ggagctgcag tgggtgctgg agctgttgc ggtaccctgg 900  
ttggactggg gttgctggct gggctggcc tcttgtacca ccggccgggc 950  
aaggccctgg aggagccagc caatgatatac aaggaggatg ccattgctcc 1000  
ccggaccctg ccctggccca agagctcaga cacaatctcc aagaatggga 1050  
cccttcctc tgtcacccccc gcacgagccc tccggccacc ccatggccct 1100  
cccaggcctg gtgcattgac cccacgccc agtctctcca gccaggccct 1150  
gccctcacca agactgcccc caacatggg gggccaccct caaccaatat 1200  
cccccatccc tggtggggtt tcttccatcg gctttagccg catgggtgct 1250  
gtgcctgtga tggtgccctgc ccagagtcaa gctggcttc tggatgtatg 1300  
acccaccac tcattggcta aaggatttgg ggtctctcc tccatataagg 1350  
gtcacctcta gcacagaggg ctgagtcatg ggaaagagtc acactcctga 1400  
cccttagtac tctgccccca cctctttta ctgtggaaaa accatctcag 1450  
taagacctaa gtgtccagga gacagaagga gaagaggaag tggatctgg 1500  
attgggagga gcctccaccc acccctgact cctccttatg aagccagctg 1550  
ctgaaattag ctactcacca agagtgggg gcagagactt ccagtcactg 1600  
agtctccctg gcccccttga tctgtacccc acccctatct aacaccaccc 1650

ttggctcca ctccagctcc ctgtattgat ataacctgac aggctggc 1700  
ggtaggttt tactggggca gaggataggg aatctttat taaaactaac 1750  
atgaaatatg tggtgtttc atttgcaa attaataaag atacataatg 1800  
tttgatgaa aaa 1813

<210> 110  
<211> 390  
<212> PRT  
<213> Homo Sapien

<400> 110  
Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe  
1 5 10 15  
Leu Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln  
20 25 30  
Leu Gln Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly  
35 40 45  
Gly Glu Val Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val  
50 55 60  
Ser Ser Ser Gln Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe  
65 70 75  
Lys Gln Lys Glu Lys Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly  
80 85 90  
Val Thr Thr Ser Lys Pro Gly Val Ser Leu Val Tyr Ser Met Pro  
95 100 105  
Ser Arg Asn Leu Ser Leu Arg Leu Glu Gly Leu Gln Glu Lys Asp  
110 115 120  
Ser Gly Pro Tyr Ser Cys Ser Val Asn Val Gln Asp Lys Gln Gly  
125 130 135  
Lys Ser Arg Gly His Ser Ile Lys Thr Leu Glu Leu Asn Val Leu  
140 145 150  
Val Pro Pro Ala Pro Pro Ser Cys Arg Leu Gln Gly Val Pro His  
155 160 165  
Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser Pro Arg Ser Lys  
170 175 180  
Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro Ser Phe Gln  
185 190 195  
Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser Leu Ser  
200 205 210  
Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys Lys  
215 220 225

Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu  
230 235 240

Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val  
245 250 255

Gly Thr Leu Val Gly Leu Gly Leu Ala Gly Leu Val Leu Leu  
260 265 270

Tyr His Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile  
275 280 285

Lys Glu Asp Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser  
290 295 300

Ser Asp Thr Ile Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser  
305 310 315

Ala Arg Ala Leu Arg Pro Pro His Gly Pro Pro Arg Pro Gly Ala  
320 325 330

Leu Thr Pro Thr Pro Ser Leu Ser Ser Gln Ala Leu Pro Ser Pro  
335 340 345

Arg Leu Pro Thr Thr Asp Gly Ala His Pro Gln Pro Ile Ser Pro  
350 355 360

Ile Pro Gly Gly Val Ser Ser Ser Gly Leu Ser Arg Met Gly Ala  
365 370 375

Val Pro Val Met Val Pro Ala Gln Ser Gln Ala Gly Ser Leu Val  
380 385 390

<210> 111  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 111  
agggtctcca ggagaaaagac tc 22

<210> 112  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 112  
atttgtggcc ttgcagacat agac 24

<210> 113  
<211> 50  
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 113

ggccacagca tcaaaacctt agaactcaat gtactggttc ctccagctcc 50

<210> 114

<211> 2479

<212> DNA

<213> Homo Sapien

<400> 114

acctgcccattt acctgttgcg agtgtggaaa aattctccct gttgaatttt 50

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gctggagttc tggacttcaa cagaacccca tccagtctt ttgattttgc 200

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ccgtacttca gaaatgggcc tacagaccac aaagtggccc agccatgggg 300

ctttttccctt gaagtcttgg cttatcattt ccctggggctt ctactcacag 350

gtgtccaaac tcctggcctg cccttagtgc tgccgctgcg acaggaactt 400

tgtctactgt aatgagcgaa gcttgacctc agtgcctttt gggatccgg 450

agggcgtaac cgtaacttac ctccacaaca accaaattaa taatgctgga 500

tttcctgcag aactgcacaa tgtacagtgc gtgcacacgg tctacctgta 550

tggcaaccaa ctggacgaat tccccatgaa cttcccaag aatgtcagag 600

ttctccattt gcaggaaaac aatattcaga ccatttcacg ggctgctttt 650

gcccgctct tgaagcttga agagctgcac ctggatgaca actccatatac 700

cacagtgggg gtggaaagacg gggccttccg ggaggctatt agcctcaaatt 750

tgttgtttt gtctaagaat cacctgagca gtgtgcctgt tggccttcc 800

gtggacttgc aagagctgag agtggatgaa aatcgaattt ctgtcatatac 850

cgacatggcc ttccagaatc tcacgagctt ggagcgtttt attgtggacg 900

ggaaccttcc gaccaacaag ggtatcgccg agggcacctt cagccatctc 950

accaagctca aggaattttc aattgtacgt aattcgctgt cccaccctcc 1000

tcccgatctc ccaggtacgc atctgatcag gctctattt caggacaacc 1050

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<210> 115  
<211> 660

<212> PRT

<213> Homo Sapien

<400> 115

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	20						25						30	
Ser	Lys	Leu	Leu	Ala	Cys	Pro	Ser	Val	Cys	Arg	Cys	Asp	Arg	Asn
	35						40					45		
Phe	Val	Tyr	Cys	Asn	Glu	Arg	Ser	Leu	Thr	Ser	Val	Pro	Leu	Gly
	50						55					60		
Ile	Pro	Glu	Gly	Val	Thr	Val	Leu	Tyr	Leu	His	Asn	Asn	Gln	Ile
	65						70					75		
Asn	Asn	Ala	Gly	Phe	Pro	Ala	Glu	Leu	His	Asn	Val	Gln	Ser	Val
	80						85					90		
His	Thr	Val	Tyr	Leu	Tyr	Gly	Asn	Gln	Leu	Asp	Glu	Phe	Pro	Met
	95						100					105		
Asn	Leu	Pro	Lys	Asn	Val	Arg	Val	Leu	His	Leu	Gln	Glu	Asn	Asn
	110						115					120		
Ile	Gln	Thr	Ile	Ser	Arg	Ala	Ala	Leu	Ala	Gln	Leu	Leu	Lys	Leu
	125						130					135		
Glu	Glu	Leu	His	Leu	Asp	Asp	Asn	Ser	Ile	Ser	Thr	Val	Gly	Val
	140						145					150		
Glu	Asp	Gly	Ala	Phe	Arg	Glu	Ala	Ile	Ser	Leu	Lys	Leu	Leu	Phe
	155						160					165		
Leu	Ser	Lys	Asn	His	Leu	Ser	Ser	Val	Pro	Val	Gly	Leu	Pro	Val
	170						175					180		
Asp	Leu	Gln	Glu	Leu	Arg	Val	Asp	Glu	Asn	Arg	Ile	Ala	Val	Ile
	185						190					195		
Ser	Asp	Met	Ala	Phe	Gln	Asn	Leu	Thr	Ser	Leu	Glu	Arg	Leu	Ile
	200						205					210		
Val	Asp	Gly	Asn	Leu	Leu	Thr	Asn	Lys	Gly	Ile	Ala	Glu	Gly	Thr
	215						220					225		
Phe	Ser	His	Leu	Thr	Lys	Leu	Lys	Glu	Phe	Ser	Ile	Val	Arg	Asn
	230						235					240		
Ser	Leu	Ser	His	Pro	Pro	Pro	Asp	Leu	Pro	Gly	Thr	His	Leu	Ile
	245						250					255		
Arg	Leu	Tyr	Leu	Gln	Asp	Asn	Gln	Ile	Asn	His	Ile	Pro	Leu	Thr
	260						265					270		

Ala Phe Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn  
 275 280 285  
 Asn Gln Leu Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser  
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 Asn Leu Lys Gln Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp  
 305 310 315  
 Cys Ser Ile Lys Trp Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser  
 320 325 330  
 Ser Leu Asn Val Arg Gly Phe Met Cys Gln Gly Pro Glu Gln Val  
 335 340 345  
 Arg Gly Met Ala Val Arg Glu Leu Asn Met Asn Leu Leu Ser Cys  
 350 355 360  
 Pro Thr Thr Thr Pro Gly Leu Pro Leu Phe Thr Pro Ala Pro Ser  
 365 370 375  
 Thr Ala Ser Pro Thr Thr Gln Pro Pro Thr Leu Ser Ile Pro Asn  
 380 385 390  
 Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro Thr Thr Ser Lys Leu  
 395 400 405  
 Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg Val Thr Pro Pro  
 410 415 420  
 Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val Asn Asp Thr  
 425 430 435  
 Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met Ala Tyr  
 440 445 450  
 Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly Ile  
 455 460 465  
 Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu  
 470 475 480  
 Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro  
 485 490 495  
 Leu Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser  
 500 505 510  
 Glu Ala Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr  
 515 520 525  
 Ala Ser Ser His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro  
 530 535 540  
 Phe Leu Leu Ala Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu  
 545 550 555  
 Val Val Leu Leu Ser Val Phe Cys Trp His Met His Lys Lys Gly

560	565	570
Arg Tyr Thr Ser Gln Lys Trp Lys Tyr Asn Arg Gly Arg Arg Lys 575	580	585
Asp Asp Tyr Cys Glu Ala Gly Thr Lys Lys Asp Asn Ser Ile Leu 590	595	600
Glu Met Thr Glu Thr Ser Phe Gln Ile Val Ser Leu Asn Asn Asp 605	610	615
Gln Leu Leu Lys Gly Asp Phe Arg Leu Gln Pro Ile Tyr Thr Pro 620	625	630
Asn Gly Gly Ile Asn Tyr Thr Asp Cys His Ile Pro Asn Asn Met 635	640	645
Arg Tyr Cys Asn Ser Ser Val Pro Asp Leu Glu His Cys His Thr 650	655	660

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<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

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<210> 117  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 117  
gcaggacaac cagataaaacc ac 22

<210> 118  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 118  
acgcagattt gagaaggctg tc 22

<210> 119  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe  
  
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ttcacgggct gctcttgccc agctcttcaa gcttgaagag ctgcac 46  
  
<210> 120  
<211> 2857  
<212> DNA  
<213> Homo Sapien  
  
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actgctgcgt tttatgttgg gaattcctct cctatggcct tgtcttggag 100  
caacagaaaa ctctcaaaca aagaaaagtca agcagccagt gcgatctcat 150  
ttgagagtga agcgtggctg ggtgtggAAC caatTTTtG taccagagga 200  
aatgaatacg actagtcatc acatcggcca gctaagatct gatttagaca 250  
atggaaacaa ttctttccag tacaagcttt tgggagctgg agctggaagt 300  
acttttatca ttgatgaaag aacaggtgac atatatgccA tacagaagct 350  
tgatagagag gagcgatccc tctacatctt aagagcccAG gtaatagaca 400  
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tcggatatacA atgacaatga accaaaattc ctagatgaac cttatgaggc 500  
cattgtacca gagatgtctc cagaaggaac attagttatc caggtgacag 550  
caagtgtatgc tgacgatccc tcaagtggta ataatgctcg tctcctctac 600  
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cataagaata tcttctaaaaa tggatagaga actgcaagat gagtattggg 700  
taatcattca agccaaaggac atgattggtc agccaggagc gttgtctgga 750  
acaacaagtg tattaattaa actttcagat gttaatgaca ataagcctat 800  
attnaaagaa agtttatacc gcttgactgt ctctgaatct gcacccactg 850  
ggacttctat aggaacaatc atggcatatg ataatgacat aggagagaat 900  
gcagaaaatgg attacagcat tgaagaggat gattcgaaa catttgacat 950  
tattactaat catgaaaactc aagaaggaat agttatatta aaaaagaaag 1000  
tggatTTGA gcaccagaac cactacggta tttagagcaa agttaaaaac 1050  
catcatgttc ctgagcagct catgaagtac cacactgagg cttccaccac 1100  
tttcattaag atccagggtgg aagatgttga tgagcctctt ctttcctcc 1150

HUMAN GENOME

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gtaggcgtgg tgtctgccac agacccagac aatagggaaat ctcctatcg 1250  
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cttccatgg gattcaagac agaagttatc attgctattc tcatttgcatt 1850  
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gaaaacagat tctatttcct gagaaaaatg aagatttcag agagaatata 1950  
ttccaatatg atgatgaagg gggggagaa gaagatacag aggctttga 2000  
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cgagaaaatt taaaggagca aaaatttgca agtcaaatacg aaatgtacaa 2750  
atcgagataa catttacatt tctatcatat tgacatgaaa attgaaaatg 2800  
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attnaaa 2857

<210> 121  
<211> 772  
<212> PRT  
<213> Homo Sapien

<400> 121  
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20 25 30  
Val Lys Gln Pro Val Arg Ser His Leu Arg Val Lys Arg Gly Trp  
35 40 45  
Val Trp Asn Gln Phe Phe Val Pro Glu Glu Met Asn Thr Thr Ser  
50 55 60  
His His Ile Gly Gln Leu Arg Ser Asp Leu Asp Asn Gly Asn Asn  
65 70 75  
Ser Phe Gln Tyr Lys Leu Leu Gly Ala Gly Ala Gly Ser Thr Phe  
80 85 90  
Ile Ile Asp Glu Arg Thr Gly Asp Ile Tyr Ala Ile Gln Lys Leu  
95 100 105  
Asp Arg Glu Glu Arg Ser Leu Tyr Ile Leu Arg Ala Gln Val Ile  
110 115 120  
Asp Ile Ala Thr Gly Arg Ala Val Glu Pro Glu Ser Glu Phe Val  
125 130 135  
Ile Lys Val Ser Asp Ile Asn Asp Asn Glu Pro Lys Phe Leu Asp  
140 145 150  
Glu Pro Tyr Glu Ala Ile Val Pro Glu Met Ser Pro Glu Gly Thr  
155 160 165  
Leu Val Ile Gln Val Thr Ala Ser Asp Ala Asp Asp Pro Ser Ser  
170 175 180  
Gly Asn Asn Ala Arg Leu Leu Tyr Ser Leu Leu Gln Gly Gln Pro  
185 190 195  
Tyr Phe Ser Val Glu Pro Thr Thr Gly Val Ile Arg Ile Ser Ser

200	205	210
Lys Met Asp Arg Glu Leu Gln Asp Glu Tyr Trp Val Ile Ile Gln		
215	220	225
Ala Lys Asp Met Ile Gly Gln Pro Gly Ala Leu Ser Gly Thr Thr		
230	235	240
Ser Val Leu Ile Lys Leu Ser Asp Val Asn Asp Asn Lys Pro Ile		
245	250	255
Phe Lys Glu Ser Leu Tyr Arg Leu Thr Val Ser Glu Ser Ala Pro		
260	265	270
Thr Gly Thr Ser Ile Gly Thr Ile Met Ala Tyr Asp Asn Asp Ile		
275	280	285
Gly Glu Asn Ala Glu Met Asp Tyr Ser Ile Glu Glu Asp Asp Ser		
290	295	300
Gln Thr Phe Asp Ile Ile Thr Asn His Glu Thr Gln Glu Gly Ile		
305	310	315
Val Ile Leu Lys Lys Lys Val Asp Phe Glu His Gln Asn His Tyr		
320	325	330
Gly Ile Arg Ala Lys Val Lys Asn His His Val Pro Glu Gln Leu		
335	340	345
Met Lys Tyr His Thr Glu Ala Ser Thr Thr Phe Ile Lys Ile Gln		
350	355	360
Val Glu Asp Val Asp Glu Pro Pro Leu Phe Leu Leu Pro Tyr Tyr		
365	370	375
Val Phe Glu Val Phe Glu Glu Thr Pro Gln Gly Ser Phe Val Gly		
380	385	390
Val Val Ser Ala Thr Asp Pro Asp Asn Arg Lys Ser Pro Ile Arg		
395	400	405
Tyr Ser Ile Thr Arg Ser Lys Val Phe Asn Ile Asn Asp Asn Gly		
410	415	420
Thr Ile Thr Thr Ser Asn Ser Leu Asp Arg Glu Ile Ser Ala Trp		
425	430	435
Tyr Asn Leu Ser Ile Thr Ala Thr Glu Lys Tyr Asn Ile Glu Gln		
440	445	450
Ile Ser Ser Ile Pro Leu Tyr Val Gln Val Leu Asn Ile Asn Asp		
455	460	465
His Ala Pro Glu Phe Ser Gln Tyr Tyr Glu Thr Tyr Val Cys Glu		
470	475	480
Asn Ala Gly Ser Gly Gln Val Ile Gln Thr Ile Ser Ala Val Asp		
485	490	495

Arg Asp Glu Ser Ile Glu Glu His His Phe Tyr Phe Asn Leu Ser  
 500 505 510  
 Val Glu Asp Thr Asn Asn Ser Ser Phe Thr Ile Ile Asp Asn Gln  
 515 520 525  
 Asp Asn Thr Ala Val Ile Leu Thr Asn Arg Thr Gly Phe Asn Leu  
 530 535 540  
 Gln Glu Glu Pro Val Phe Tyr Ile Ser Ile Leu Ile Ala Asp Asn  
 545 550 555  
 Gly Ile Pro Ser Leu Thr Ser Thr Asn Thr Leu Thr Ile His Val  
 560 565 570  
 Cys Asp Cys Gly Asp Ser Gly Ser Thr Gln Thr Cys Gln Tyr Gln  
 575 580 585  
 Glu Leu Val Leu Ser Met Gly Phe Lys Thr Glu Val Ile Ile Ala  
 590 595 600  
 Ile Leu Ile Cys Ile Met Ile Ile Phe Gly Phe Ile Phe Leu Thr  
 605 610 615  
 Leu Gly Leu Lys Gln Arg Arg Lys Gln Ile Leu Phe Pro Glu Lys  
 620 625 630  
 Ser Glu Asp Phe Arg Glu Asn Ile Phe Gln Tyr Asp Asp Glu Gly  
 635 640 645  
 Gly Gly Glu Glu Asp Thr Glu Ala Phe Asp Ile Ala Glu Leu Arg  
 650 655 660  
 Ser Ser Thr Ile Met Arg Glu Arg Lys Thr Arg Lys Thr Thr Ser  
 665 670 675  
 Ala Glu Ile Arg Ser Leu Tyr Arg Gln Ser Leu Gln Val Gly Pro  
 680 685 690  
 Asp Ser Ala Ile Phe Arg Lys Phe Ile Leu Glu Lys Leu Glu Glu  
 695 700 705  
 Ala Asn Thr Asp Pro Cys Ala Pro Pro Phe Asp Ser Leu Gln Thr  
 710 715 720  
 Tyr Ala Phe Glu Gly Thr Gly Ser Leu Ala Gly Ser Leu Ser Ser  
 725 730 735  
 Leu Glu Ser Ala Val Ser Asp Gln Asp Glu Ser Tyr Asp Tyr Leu  
 740 745 750  
 Asn Glu Leu Gly Pro Arg Phe Lys Arg Leu Ala Cys Met Phe Gly  
 755 760 765  
 Ser Ala Val Gln Ser Asn Asn  
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<210> 122

<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 122  
cttgactgtc tctgaatctg caccc 25

<210> 123  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 123  
aagtgggtgga agcctccagt gtgg 24

<210> 124  
<211> 52  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 124  
ccactacggt attagagcaa aagttaaaaa ccatcatggt tcctggagca 50

gc 52

<210> 125  
<211> 1152  
<212> DNA  
<213> Homo Sapien

<400> 125  
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gtctgcaatg gcccgcctgc agaaaatctgt gagctcttc cttatgggaa 100  
ccctggccac cagctgcctc cttctttgg cccttttgtt acagggagga 150  
gcagctgcgc ccatcagctc ccactgcagg cttgacaagt ccaacttcca 200  
gcagccctat atcaccaacc gcaccttcat gctggctaag gaggctagct 250  
tggctgataa caacacagac gttcgtctca ttggggagaa actgttccac 300  
ggagtcagta tgagtgagcg ctgctatctg atgaagcagg tgctgaactt 350  
cacccctgaa gaagtgttgt tccctcaatc tgataggttc cagccttata 400  
tgcaggaggt ggtgcccttc ctggccaggg tcagcaacag gctaagcaca 450

tgtcatattg aaggtgatga cctgcatac cagaggaatg tgcaaaagct 500  
gaaggacaca gtaaaaaagc ttggagagag tggagagatc aaagcaattg 550  
gagaactgga tttgctgtt atgtctctga gaaatgcctg catttgacca 600  
gagcaaagct gaaaaatgaa taactaaccc cctttccctg ctagaaataa 650  
caatttagatg ccccaaagcg atttttta accaaaagga agatgggaag 700  
ccaaactcca tcatgatggg tggattccaa atgaaccct gcgttagtta 750  
caaaggaaac caatgccact tttgtttata agaccagaag gtagactttc 800  
taagcataga tatttattga taacatttca ttgtaactgg tggctatac 850  
acagaaaaca atttatttt taaataattg tcttttcca taaaaaaagat 900  
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ataatcagta ctatatatattt ataaatgtat ttattattat tataagactg 1000  
cattttatattt atatcatttt attaatatgg atttatttat agaaacatca 1050  
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attatagagc tataacatgt ttatggacc tcaataaaca cttggatatac 1150  
cc 1152

<210> 126  
<211> 179  
<212> PRT  
<213> Homo Sapien

<400> 126  
Met Ala Ala Leu Gln Lys Ser Val Ser Ser Phe Leu Met Gly Thr  
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Leu Ala Thr Ser Cys Leu Leu Leu Ala Leu Leu Val Gln Gly  
20 25 30  
Gly Ala Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser  
35 40 45  
Asn Phe Gln Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala  
50 55 60  
Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile  
65 70 75  
Gly Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys Tyr  
80 85 90  
Leu Met Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe  
95 100 105  
Pro Gln Ser Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro

110	115	120
Phe Leu Ala Arg Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu		
125	130	135
Gly Asp Asp Leu His Ile Gln Arg Asn Val Gln Lys Leu Lys Asp		
140	145	150
Thr Val Lys Lys Leu Gly Glu Ser Gly Glu Ile Lys Ala Ile Gly		
155	160	165
Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn Ala Cys Ile		
170	175	

<210> 127  
<211> 2557  
<212> DNA  
<213> Homo Sapien

<400> 127  
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tagtggatct ggggcaggca gcggcgctgg ctgtggatt agatctgttt 250  
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caagtggctt ctcctccctt cgggtttgt tcagtgtcgg gtgagggttg 400  
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<210> 128  
<211> 529  
<212> PRT  
<213> Homo Sapien

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Lys Pro Gly Asp Gln Ile Leu Asp Trp Gln Tyr Gly Val Thr Gln  
35 40 45  
Ala Phe Pro His Thr Glu Glu Glu Val Glu Val Asp Ser His Ala  
50 55 60  
Tyr Ser His Arg Trp Lys Arg Asn Leu Asp Phe Leu Lys Ala Val  
65 70 75  
Asp Thr Asn Arg Ala Ser Val Gly Gln Asp Ser Pro Glu Pro Arg  
80 85 90  
Ser Phe Thr Asp Leu Leu Leu Asp Asp Gly Gln Asp Asn Asn Thr  
95 100 105  
Gln Ile Glu Glu Asp Thr Asp His Asn Tyr Tyr Ile Ser Arg Ile  
110 115 120  
Tyr Gly Pro Ser Asp Ser Ala Ser Arg Asp Leu Trp Val Asn Ile  
125 130 135  
Asp Gln Met Glu Lys Asp Lys Val Lys Ile His Gly Ile Leu Ser  
140 145 150  
Asn Thr His Arg Gln Ala Ala Arg Val Asn Leu Ser Phe Asp Phe  
155 160 165  
Pro Phe Tyr Gly His Phe Leu Arg Glu Ile Thr Val Ala Thr Gly  
170 175 180  
Gly Phe Ile Tyr Thr Gly Glu Val Val His Arg Met Leu Thr Ala  
185 190 195  
Thr Gln Tyr Ile Ala Pro Leu Met Ala Asn Phe Asp Pro Ser Val  
200 205 210  
Ser Arg Asn Ser Thr Val Arg Tyr Phe Asp Asn Gly Thr Ala Leu  
215 220 225

Val Val Gln Trp Asp His Val His Leu Gln Asp Asn Tyr Asn Leu  
                  230                     235                     240  
 Gly Ser Phe Thr Phe Gln Ala Thr Leu Leu Met Asp Gly Arg Ile  
                  245                     250                     255  
 Ile Phe Gly Tyr Lys Glu Ile Pro Val Leu Val Thr Gln Ile Ser  
                  260                     265                     270  
 Ser Thr Asn His Pro Val Lys Val Gly Leu Ser Asp Ala Phe Val  
                  275                     280                     285  
 Val Val His Arg Ile Gln Gln Ile Pro Asn Val Arg Arg Arg Thr  
                  290                     295                     300  
 Ile Tyr Glu Tyr His Arg Val Glu Leu Gln Met Ser Lys Ile Thr  
                  305                     310                     315  
 Asn Ile Ser Ala Val Glu Met Thr Pro Leu Pro Thr Cys Leu Gln  
                  320                     325                     330  
 Phe Asn Arg Cys Gly Pro Cys Val Ser Ser Gln Ile Gly Phe Asn  
                  335                     340                     345  
 Cys Ser Trp Cys Ser Lys Leu Gln Arg Cys Ser Ser Gly Phe Asp  
                  350                     355                     360  
 Arg His Arg Gln Asp Trp Val Asp Ser Gly Cys Pro Glu Glu Ser  
                  365                     370                     375  
 Lys Glu Lys Met Cys Glu Asn Thr Glu Pro Val Glu Thr Ser Ser  
                  380                     385                     390  
 Arg Thr Thr Thr Thr Val Gly Ala Thr Thr Thr Gln Phe Arg Val  
                  395                     400                     405  
 Leu Thr Thr Thr Arg Arg Ala Val Thr Ser Gln Phe Pro Thr Ser  
                  410                     415                     420  
 Leu Pro Thr Glu Asp Asp Thr Lys Ile Ala Leu His Leu Lys Asp  
                  425                     430                     435  
 Asn Gly Ala Ser Thr Asp Asp Ser Ala Ala Glu Lys Lys Gly Gly  
                  440                     445                     450  
 Thr Leu His Ala Gly Leu Ile Ile Gly Ile Leu Ile Leu Val Leu  
                  455                     460                     465  
 Ile Val Ala Thr Ala Ile Leu Val Thr Val Tyr Met Tyr His His  
                  470                     475                     480  
 Pro Thr Ser Ala Ala Ser Ile Phe Phe Ile Glu Arg Arg Pro Ser  
                  485                     490                     495  
 Arg Trp Pro Ala Met Lys Phe Arg Arg Gly Ser Gly His Pro Ala  
                  500                     505                     510  
 Tyr Ala Glu Val Glu Pro Val Gly Glu Lys Glu Gly Phe Ile Val

515

520

525

Ser Glu Gln Cys

<210> 129  
<211> 4834  
<212> DNA  
<213> Homo Sapien

<220>  
<221> unsure  
<222> 3784  
<223> unknown base

<400> 129  
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cctcctgcct cccggctgga cagagtgtgg acttcccctg ggccggccgtg 150  
gacaacatga tggtcagaaa aggggacacg gcggtgctta ggtgttattt 200  
ggaagatgga gcttcaaagg gtgcctggct gaaccggtca agtattattt 250  
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ttgaataaaa gggactacag cctccagata cagaatgttag atgtgacaga 350  
tgatggccca tacacgtgtt ctgttcagac tcaacataca cccagaacaa 400  
tgcaggtgca tctaactgtg caagttcctc ctaagatata tgacatctca 450  
aatgatatga ccgtcaatga aggaaccaac gtcactctta cttgtttggc 500  
caactggaaa ccagagcctt ccatttcttg gcgacacatc tccccatcag 550  
caaaaccatt tgaaaatgga caatatttgg acatttatgg aattacaagg 600  
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aaattaaatc tggcacccgtg accccccggac gcagtggcct gataagatgt 750  
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gatccattct cactgttacc aacgtgacac aggagcactt cgccaattat 900  
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gcactgacaa tggggttga gaattttgcc ccacactaac tcagtttttg 1900  
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aaactctgaa aaactgaatt atcaaagtca atcatctata atgatcaaat 4450  
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aaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaa 4834

<210> 130  
<211> 354  
<212> PRT  
<213> Homo Sapien

<400> 130  
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Cys Leu Pro Ala Gly Gln Ser Val Asp Phe Pro Trp Ala Ala Val  
35 40 45  
Asp Asn Met Met Val Arg Lys Gly Asp Thr Ala Val Leu Arg Cys  
50 55 60  
Tyr Leu Glu Asp Gly Ala Ser Lys Gly Ala Trp Leu Asn Arg Ser  
65 70 75  
Ser Ile Ile Phe Ala Gly Asp Lys Trp Ser Val Asp Pro Arg

80	85	90
Val Ser Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln Ile		
95	100	105
Gln Asn Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val		
110	115	120
Gln Thr Gln His Thr Pro Arg Thr Met Gln Val His Leu Thr Val		
125	130	135
Gln Val Pro Pro Lys Ile Tyr Asp Ile Ser Asn Asp Met Thr Val		
140	145	150
Asn Glu Gly Thr Asn Val Thr Leu Thr Cys Leu Ala Thr Gly Lys		
155	160	165
Pro Glu Pro Ser Ile Ser Trp Arg His Ile Ser Pro Ser Ala Lys		
170	175	180
Pro Phe Glu Asn Gly Gln Tyr Leu Asp Ile Tyr Gly Ile Thr Arg		
185	190	195
Asp Gln Ala Gly Glu Tyr Glu Cys Ser Ala Glu Asn Asp Val Ser		
200	205	210
Phe Pro Asp Val Arg Lys Val Lys Val Val Asn Phe Ala Pro		
215	220	225
Thr Ile Gln Glu Ile Lys Ser Gly Thr Val Thr Pro Gly Arg Ser		
230	235	240
Gly Leu Ile Arg Cys Glu Gly Ala Gly Val Pro Pro Pro Ala Phe		
245	250	255
Glu Trp Tyr Lys Gly Glu Lys Lys Leu Phe Asn Gly Gln Gln Gly		
260	265	270
Ile Ile Ile Gln Asn Phe Ser Thr Arg Ser Ile Leu Thr Val Thr		
275	280	285
Asn Val Thr Gln Glu His Phe Gly Asn Tyr Thr Cys Val Ala Ala		
290	295	300
Asn Lys Leu Gly Thr Thr Asn Ala Ser Leu Pro Leu Asn Pro Pro		
305	310	315
Ser Thr Ala Gln Tyr Gly Ile Thr Gly Ser Ala Asp Val Leu Phe		
320	325	330
Ser Cys Trp Tyr Leu Val Leu Thr Leu Ser Ser Phe Thr Ser Ile		
335	340	345
Phe Tyr Leu Lys Asn Ala Ile Leu Gln		
350		

<210> 131  
<211> 823

<212> DNA

<213> Homo Sapien

<400> 131

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gcataattac gaggaagcag aacttctcca gaagcaagcg cacatgcgtt 200  
ccaaaataag agcaaattcg ctctaaacac aggaaaagac ctgaagcttt 250  
aattaagggg ttacatccaa ccccagagcg cttttgtggg cactgattgc 300  
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ccaagctcca aagaagagac ccaagtcccc aaaacattga tttcaggcgt 450  
gccaggaagg aagagcagca gcaggggtggg agagaagctc cagtcagccc 500  
acaagatgcc attgtccccc ggccctctgc tgctgctgct ctccggggcc 550  
acggccaccg ctgcccgtcc cctggagggt ggccccaccg gccgagacag 600  
cgagcatatg caggaagcgg caggaataag gaaaagcagc ctcctgactt 650  
tcctcgcttg gtggtttgag tggacctccc aggccagtgc cggcccccctc 700  
ataggagagg aagctcgaaa ggtggccagg cggcaggaag ggcacccccc 750  
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agaccttctc ctccctgcaaa tag 823

<210> 132

<211> 155

<212> PRT

<213> Homo Sapien

<400> 132

Met	Tyr	Arg	His	Lys	Asn	Ser	Trp	Arg	Leu	Gly	Leu	Lys	Tyr	Pro
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Pro	Ser	Ser	Lys	Glu	Glu	Thr	Gln	Val	Pro	Lys	Thr	Leu	Ile	Ser
			20					25				30		
Gly	Leu	Pro	Gly	Arg	Lys	Ser	Ser	Ser	Arg	Val	Gly	Glu	Lys	Leu
	35							40				45		
Gln	Ser	Ala	His	Lys	Met	Pro	Leu	Ser	Pro	Gly	Leu	Leu	Leu	
			50				55				60			
Leu	Leu	Ser	Gly	Ala	Thr	Ala	Thr	Ala	Ala	Leu	Pro	Leu	Glu	Gly
	65						70				75			

Gly Pro Thr Gly Arg Asp Ser Glu His Met Gln Glu Ala Ala Gly  
80 85 90

Ile Arg Lys Ser Ser Leu Leu Thr Phe Leu Ala Trp Trp Phe Glu  
95 100 105

Trp Thr Ser Gln Ala Ser Ala Gly Pro Leu Ile Gly Glu Glu Ala  
110 115 120

Arg Glu Val Ala Arg Arg Gln Glu Gly Ala Pro Pro Gln Gln Ser  
125 130 135

Ala Arg Arg Asp Arg Met Pro Cys Arg Asn Phe Phe Trp Lys Thr  
140 145 150

Phe Ser Ser Cys Lys  
155

<210> 133

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 133

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<210> 134

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gcaggaggag aaggtttcc agaagaag 28

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 135

agaagttcca gtcagccac aagatgccat tgtccccgg cctcc 45

<210> 136

<211> 1875

<212> DNA

<213> Homo Sapien

<400> 136

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atggtaccac ctcccggaaaa tgtcagaatg aattctgtta atttcaagaa 150  
cattctacag tgggagtcac ctgctttgc caaaggaaac ctgactttca 200  
cagctcagta cctaagttat aggatattcc aagataaatg catgaatact 250  
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cttgagagtc agggctgaat ttgcagatga gcattcagac tggtaaaca 350  
tcaccttctg tcctgtggat gacaccatta ttggaccccc tggaatgcaa 400  
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ttctaccaga ttatggatgg actgatctga aaatcgacct caactcaagg 1750  
gtggtcagct caatgctaca cagagcacgg acttttggat tctttcagt 1800  
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ccattaaagt tttactctgt gttgc 1875

<210> 137

<211> 325

<212> PRT

<213> Homo Sapien

<400> 137

Met	Ala	Trp	Ser	Leu	Gly	Ser	Trp	Leu	Gly	Gly	Cys	Leu	Leu	Val
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Ser	Ala	Leu	Gly	Met	Val	Pro	Pro	Pro	Glu	Asn	Val	Arg	Met	Asn
				20				25					30	
Ser	Val	Asn	Phe	Lys	Asn	Ile	Leu	Gln	Trp	Glu	Ser	Pro	Ala	Phe
				35				40					45	
Ala	Lys	Gly	Asn	Leu	Thr	Phe	Thr	Ala	Gln	Tyr	Leu	Ser	Tyr	Arg
				50				55					60	
Ile	Phe	Gln	Asp	Lys	Cys	Met	Asn	Thr	Thr	Leu	Thr	Glu	Cys	Asp
				65				70					75	
Phe	Ser	Ser	Leu	Ser	Lys	Tyr	Gly	Asp	His	Thr	Leu	Arg	Val	Arg
					80			85					90	
Ala	Glu	Phe	Ala	Asp	Glu	His	Ser	Asp	Trp	Val	Asn	Ile	Thr	Phe
				95				100					105	
Cys	Pro	Val	Asp	Asp	Thr	Ile	Ile	Gly	Pro	Pro	Gly	Met	Gln	Val
				110				115					120	
Glu	Val	Leu	Ala	Asp	Ser	Leu	His	Met	Arg	Phe	Leu	Ala	Pro	Lys
				125				130					135	
Ile	Glu	Asn	Glu	Tyr	Glu	Thr	Trp	Thr	Met	Lys	Asn	Val	Tyr	Asn
				140				145					150	
Ser	Trp	Thr	Tyr	Asn	Val	Gln	Tyr	Trp	Lys	Asn	Gly	Thr	Asp	Glu
				155				160					165	
Lys	Phe	Gln	Ile	Thr	Pro	Gln	Tyr	Asp	Phe	Glu	Val	Leu	Arg	Asn
				170				175					180	

Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg Gly Phe Leu  
 185 190 195  
 Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu  
 200 205 210  
 Gln Thr Thr His Asp Glu Thr Val Pro Ser Trp Met Val Ala Val  
 215 220 225  
 Ile Leu Met Ala Ser Val Phe Met Val Cys Leu Ala Leu Leu Gly  
 230 235 240  
 Cys Phe Ser Leu Leu Trp Cys Val Tyr Lys Lys Thr Lys Tyr Ala  
 245 250 255  
 Phe Ser Pro Arg Asn Ser Leu Pro Gln His Leu Lys Glu Phe Leu  
 260 265 270  
 Gly His Pro His His Asn Thr Leu Leu Phe Phe Ser Phe Pro Leu  
 275 280 285  
 Ser Asp Glu Asn Asp Val Phe Asp Lys Leu Ser Val Ile Ala Glu  
 290 295 300  
 Asp Ser Glu Ser Gly Lys Gln Asn Pro Gly Asp Ser Cys Ser Leu  
 305 310 315  
 Gly Thr Pro Pro Gly Gln Gly Pro Gln Ser  
 320 325

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 <211> 2570  
 <212> DNA  
 <213> Homo Sapien

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 gcccgcgcgc ctgctggcg agatgccccg ccggggcaaaa tcgcgggtgg 150  
 tggggctggg attgggggt ctgctgtggc ccattttctc cagcagca 200  
 ttggacactcg ggtgcagatc gacgtgtacg agaaggaaac cgtgggtggc 250  
 cgcttggcca ccatctcagt caacaaggcag cactatgaga gcggggctgc 300  
 ctccttccac tccctgagcc tgcacatgca ggacttcgtc aagctgctgg 350  
 ggctgaggca ccggcgccgag gtgggtggca ggagcgccat cttcggcg 400  
 gagcacttca tgctggagga gactgactgg tacctgctga acctttccg 450  
 cctctggtgg cactatggca tcagcttcct gaggctgcag atgtgggtgg 500  
 aggaggtcat ggagaagttc atgaggatct ataagtacca ggcccacggc 550

tatgccttct cgggtgtgga ggagctgctc tactcaactgg gggagtccac 600  
ctttgttaac atgaccaggc actctgtggc tgagtccctg ctgcagggtgg 650  
gcgtcacgca gcgcatttatt gatgatgtcg tttctgtgt cctgcgggcc 700  
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agccggggcc caaggcagcc tgtggctgt ggaaggaggc aataagctgg 800  
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gcaggcttcc acccgcccat tcatgacgtg cagggcttcc tccagccac 1050  
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cagaccctaa gctttcccc tttgccaaca tccttaccac agatttcccc 1150  
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tcagtgcaga cagctgagtg gcaggccat cccctctatg gctccggccc 1350  
cacgctcccg aggtttgcac tccatgacca gctttctac ctcaatgccc 1400  
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tactgtttt cactacctac tcccacaatg gacaatcaat tgaggcaacc 1950  
tacaagaaaa catttacaac cagatggta caaataaagt agaagggaaag 2000

atcagaaaac ctaagaaatg atcatagctc ctggttactg tggacttgat 2050  
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tcaacatcac tgcatattgg aggagatgac tgtggtagga cccaaggaag 2150  
agatgtgtgc ctgaatagtc gtcaccatat ctccaagctt cctggcaacc 2200  
agtggaaaaa gaaacatgcg aggctgtagg aagagggaaag ctcttcctt 2250  
gcacctagag gaattagcca ttctttcct tatgcaaaga ttgaggaatg 2300  
caacaatata aagaagagaa gtccccagat ggtagagagc agtcatatct 2350  
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gattcttcag aggttagcct ggtactttct catcagacac tagcttgaag 2450  
taagaggaga attatgctt tcttgctt ttctacaaac cctaaaaat 2500  
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aaaaaaaaaa aaaaaaaaaa 2570

<210> 139

<211> 494

<212> PRT

<213> Homo Sapien

<400> 139

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20 25 30

Val Val Gly Ala Gly Ile Gly Gly Ser Ala Val Ala His Phe Leu  
35 40 45

Gln Gln His Phe Gly Pro Arg Val Gln Ile Asp Val Tyr Glu Lys  
50 55 60

Gly Thr Val Gly Gly Arg Leu Ala Thr Ile Ser Val Asn Lys Gln  
65 70 75

His Tyr Glu Ser Gly Ala Ala Ser Phe His Ser Leu Ser Leu His  
80 85 90

Met Gln Asp Phe Val Lys Leu Leu Gly Leu Arg His Arg Arg Glu  
95 100 105

Val Val Gly Arg Ser Ala Ile Phe Gly Gly Glu His Phe Met Leu  
110 115 120

Glu Glu Thr Asp Trp Tyr Leu Leu Asn Leu Phe Arg Leu Trp Trp  
125 130 135

His Tyr Gly Ile Ser Phe Leu Arg Leu Gln Met Trp Val Glu Glu

140	145	150
Val Met Glu Lys Phe Met Arg Ile Tyr	Lys Tyr Gln Ala His	Gly
155	160	165
Tyr Ala Phe Ser Gly Val Glu Glu Leu	Leu Tyr Ser Leu Gly	Glu
170	175	180
Ser Thr Phe Val Asn Met Thr Gln His	Ser Val Ala Glu Ser	Leu
185	190	195
Leu Gln Val Gly Val Thr Gln Arg Phe	Ile Asp Asp Val Val	Ser
200	205	210
Ala Val Leu Arg Ala Ser Tyr Gly Gln	Ser Ala Ala Met Pro	Ala
215	220	225
Phe Ala Gly Ala Met Ser Leu Ala Gly	Ala Gln Gly Ser Leu	Trp
230	235	240
Ser Val Glu Gly Gly Asn Lys Leu Val	Cys Ser Gly Leu Leu	Lys
245	250	255
Leu Thr Lys Ala Asn Val Ile His Ala	Thr Val Thr Ser Val	Thr
260	265	270
Leu His Ser Thr Glu Gly Lys Ala Leu	Tyr Gln Val Ala Tyr	Glu
275	280	285
Asn Glu Val Gly Asn Ser Ser Asp Phe	Tyr Asp Ile Val Val	Ile
290	295	300
Ala Thr Pro Leu His Leu Asp Asn Ser	Ser Ser Asn Leu Thr	Phe
305	310	315
Ala Gly Phe His Pro Pro Ile Asp Asp	Val Gln Gly Ser Phe	Gln
320	325	330
Pro Thr Val Val Ser Leu Val His Gly	Tyr Leu Asn Ser Ser	Tyr
335	340	345
Phe Gly Phe Pro Asp Pro Lys Leu Phe	Pro Phe Ala Asn Ile	Leu
350	355	360
Thr Thr Asp Phe Pro Ser Phe Phe Cys	Thr Leu Asp Asn Ile	Cys
365	370	375
Pro Val Asn Ile Ser Ala Ser Phe Arg	Arg Lys Gln Pro Gln	Glu
380	385	390
Ala Ala Val Trp Arg Val Gln Ser Pro	Lys Pro Leu Phe Arg	Thr
395	400	405
Gln Leu Lys Thr Leu Phe Arg Ser Tyr	Tyr Ser Val Gln Thr	Ala
410	415	420
Glu Trp Gln Ala His Pro Leu Tyr Gly	Ser Arg Pro Thr Leu	Pro
425	430	435

Arg Phe Ala Leu His Asp Gln Leu Phe Tyr Leu Asn Ala Leu Glu  
440 445 450

Trp Ala Ala Ser Ser Val Glu Val Met Ala Val Ala Ala Lys Asn  
455 460 465

Val Ala Leu Leu Ala Tyr Asn Arg Trp Tyr Gln Asp Leu Asp Lys  
470 475 480

Ile Asp Gln Lys Asp Leu Met His Lys Val Lys Thr Glu Leu  
485 490

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<210> 141  
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cacaaactcg aactgcttct g 21

<210> 148  
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<212> DNA  
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<210> 151  
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